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            Sequence 39, Appl
Patent No. 5171685
Patent No. 5171685
Sequence 37, Appl
Sequence 13, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.5%; Score 83; DB 1; Length 15; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No.
STREET: One Liberty Place 46th Floor
PCT-US95-04018-53
US-08-856-074A-39
                        5171685-7
5518316-7
02-08-812-829-29
PCT-US92-10432-1
US-08-442-542-43
US-08-442-542-43
US-08-366-591-15
US-08-366-591-15
US-08-288-059-7
US-08-288-059-7
US-08-361-920-13
US-08-479-939-13
US-08-479-939-13
US-08-471-033-47
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; Sequence 56, Application US/08221583
; Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                            1711163153366
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Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: WOOGCOCK W
STREET: One Liberty P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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MOLECULE TYPE: peptide
US-08-221-583-56
 14444933344441
14444936337774469
1444493633777479
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CLASSIFICATION: 514
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GENERAL INFORMATION:
LENGTH:
RESULT
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                                                                                                             (without alignments)
102.779 Million cell updates/sec
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                                                                                                February 12, 2002, 12:58:25; Search time 12.48 Seconds
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1 TSTSPTRSMAPGAVHLPQPV......STSFLLPMGPSPPAEGSTGD
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         Ltd.
          GenCore version 4.5
(c) 1993 - 2000 Compugen
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PCT-US95-04018-56
US-08-221-583-58
US-08-221-583-57
US-08-221-583-57
PCT-US95-04018-55
PCT-US95-04018-55
PCT-US95-04018-55
PCT-US95-04018-55
PCT-US95-04018-55
PCT-US95-04018-56
PCT-US95-04018-59
PCT-US95-04018-59
PCT-US95-04018-59
PCT-US95-04018-61
US-08-221-583-61
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US - 08 - 361 - 920 - 19
US - 08 - 479 - 939 - 19
US - 08 - 483 - 432 - 19
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US-08-467-282B-44
US-08-471-282A-44
US-08-466-710C-44
US-08-468-739C-44
US-08-221-583-53
                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
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                                                                                                                                                         us-09-800-909-2_coPY_201_257
                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                     protein search, using sw model
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
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Match Length
                         Copyright
                                                                                                                                                                                                                                                                                                                      length: 0
length: 57
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Maximum DB seq
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                                                                                                                                                                        score:
                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number
                                                                   protein
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                        Title:
Perfect :
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24 SQHTQPTPEPSTAPS 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-04018-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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Sequence 58, Application US/08221583
Sequence 58, Application US/08221583
Sequence 58, Application US/08221583
Sequence 58, Application US/08221583
Sequence 58, Application: Tenance Application: APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Macklewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STRATE:, Pennsylvania
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0
       Sequence 56, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Webert, Marian
APPLICANT: Webert, Nobert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wordsock Washburn Kurtz Mackiewicz &
ADDRESSEE: Wordsock Washburn Kurtz Philadelphia
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STARE: Ponnesulvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.5%; Score 83; DB 5; Length 15; 100.0%; Pred. No. 0.0037;
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                                                                                                                                                                                                                                                                                                                                                               ZIP: 19403

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WOLDFORM: PC-DOS/MS-DOS
SOFTWARE: WOLDFORM: PC-DOS/MS-DOS
SOFTWARE: WOLDFORM: PC-LOS/MS-DOS
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCORTELECOMMUNICATION INFORMATION:
TELEFOMMUNICATION 1015) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SED ID NO: 56: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 HLPQPVSTRSQHTQP 29
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                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PCT-US95-04018-56
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Gaps
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                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Le.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 82; DB 100.0%; Pred. No. 0.0
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                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568 3130
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION WUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
RPLICATION WUMBER: US 08/221,581
FILING DATE: 01-APR-1994
APPLICATION WUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDHORFOCT 5.1 CURRENY APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04018
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 27.2
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-221-583-58
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Gaps
                                                                                                   APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: WoodCock Washburn Kurtz Macklewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod. CURRENT APPLICATION DATA:
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Pred. No. 0.006;
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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Mervier, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOOGGOCK Washburn Kurtz Macklewicz 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      Sequence 62, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGIETRATTON UNUMBER: 33,229
REFERENCE/DOCKET UNUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
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MOLECULE TYPE: peptide
US-08-221-583-62
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Liberty
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                               STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                         19403
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PCT-US95-04018-57
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RESULT 6
US-08-221-583-62
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE Mashburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                        27.2%; Score 82; DB 5; Length 15; 100.0%; Pred. No. 0.0047; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 81; DB 1; Length 15; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
                REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3400
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
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REGISTRATION NUMBER: 33,229
REPERENCE/DOCKET NUMBER: CCOR-
TELEDOMUNICATION INFORMATION:
TELEPANE: (215) 568-3100
TELEPAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57;
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 amino acids
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Matches 15; Conservative
                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide
PCT-US95-04018-58
                                                                                                                                                                                                                                                                                                                                                                                                                  1 SQHTQPTPEPSTAPS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 STRSQHTQPTPEPST 35
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                                                                                                                                                                                                         linear
                                                                                                                                                                                                      TOPOLOGY:
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US-08-221-583-57
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Gaps
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.5%; Score 80; DB 1; Length 15; 100.0%; Pred. No. 0.0077; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                        DB 5; Leus
1. 0.006;
0;
                                                                                                                                                                                                                                                                                                                           26.8%; Sco. 100.0%; Pred. No. v. 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3409
INFORMATION FOR SEQ ID NO: 55:
                                                                CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/08221583 Patent No. 5486595 GENERAL INFORMATION:
                                                          REFERENCE/DOCKET NUMBER: CCOR TELECOMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS: LENTH: 15 amino acids TYPE: amino acid
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide PCT-US95-04018-62
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-221-583-55
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 81; DB 5; Length 15; 100.0%; Pred. No. 0.006; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,580
APPLICATION NUMBER: US 08/221,583
FLING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: DELUCA, MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFMARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
  PCT/US95/04018
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FORT-1059-4018-62
Sequence 62, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Philadelphia
STATE: Pennsylvania
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Matches 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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26.5%; Score 80; DB 5; Length 15; 100.0%; Pred. No. 0.0077; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibito
OVRRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania
                                                          CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA MARK
REGISTRATION NUMBER: 33,229
BREFERENER/DACKET NIMBER: CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
                   APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CCOF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.5
Best Local Similarity 100.
Matches 15; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide
PCT-US95-04018-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GAVHLPQPVSTRSQH 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: Bennsylvania COUNTRY: ID403

COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPASSIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%; Score 80; DB 1; Length 15; 100.0%; Pred. No. 0.0077; Live 0; Mismatches 0; Indels
                                                  Sequence 59, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Necrosis Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty Place 46th Floor CITY: Philadelphia
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTATION UNDRER: 33,229
REFERENCE/DOCKET UNDRER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necros
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.5
Best Local Similarity 100.
Matches 15; Conservative
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MOLECULE TYPE: peptide
US-08-221-583-59
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
3Y: linear
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PCT-US95-04018-55
                                      US-08-221-583-59
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Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB 5; Pred. No. 0.0098;
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                                                                                                                                                                                                                                                                                                         STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: O1-APR-1994
ATPONREY/AGRAT INFORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHIONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US95/04018
                                                                                Sequence 61, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mcriszynski, Marian
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.2%; SCC.
100.0%; Pre
0; }
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 PSTAPSTSFLLPMGP 47
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             19403
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
UNBRER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                             ;
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SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 5; Length 15;
Pred. No. 0.0077;
0; Mismatches 0; Indels
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Pred. No. 0.0098;
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                                                                              REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEFRAN: (215) 568-3409
TELEFAX: (215) 568-3499
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/08221583 Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                     26.5%; Sco.
100.0%; Pre
0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                     NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
FILING DATE: 01-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: (
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                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
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                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-59
                                                                                                                                                                                                                                                                                                                                                                                                                                 27 TOPTPEPSTAPSTSF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TQPTPEPSTAPSTSF 15
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches, 15; Conserva
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                                                                                                                                                                                                                                 TYPE: amino acid
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APPLICANT: Heavne.
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STATE:
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STREÉT: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Search completed: February 12, 2002, 13:00:17 Job time: 112 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

; Search time 19.28 Seconds February 12, 2002, 12:45:58

(without alignments) 1821.394 Million cell updates/sec

1 MAPVAVWAALAVGLELWAAA......GSTEEKPLPLGVPDAGMKPS 461 US-09-800-909-2 2468 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

219241

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description		tumor necrosis fac	gene murine tumour	G2R protein - vari	hypothetical prote	gene G4R protein -	T2 protein - myxom	osi	T2 protein - rabbi	B-cell activation	-H	nerve growth facto		len	gene ox40 protein	membrane glycoprot	OX40 homolog - hum	nerve growth facto	necrosis	T-cell antigen 4-1	Ø	tumor necrosis fac	tumor necrosis fac	lymphocyte activat	tumor necrosis fac	glucan 1,4-alpha-g	N	4	hypothetical prote
SUMMARIES																														
SUM	di	A35356	B38634	I48854	D72175	T28623	D36858	GOVZML	I54182	B43692	A60771	A46476	JN000K	A42086	S12783	148700	JC5486	137552	GOHUN	JC4302	B32393	A26431	GOMST1	GQRTT1	138426	GQHUT1	S48478	22	74	T25933
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	Length I	461	474	459	349	348	349	326	435	325	277	305	416	595	271	272	493	277	427	461	256	425	454	461	255	455	1367	770	1203	1372
dР	Query	0	61.3	59.8	15.5	15.4	S	4	13.8	ش	12.9		。						8.5								•	٠	6.5	•
	Score	46	1512	~		379.5				328	317.5	258.5	251.5	241	229.5	223.5	219.5	217	210	198	197	197	191.5	185.5	185	183.5	166.5	16	٠	161
	Result No.	-	7	٣	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

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159.5 156.5 156.5 154.5 154.5 148.5 148.5 147 147 143.4	143	. 143	142
330 330 330 444 441 450	e	44	45

ALIGNMENTS

RESULT

A35356 A35456 A35456 A35456 A35456 A35456 A35456 A35456 A3646 A3646 A3646 A36476 A3647
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Proc. Natl. Acad. Sci. U.S.A. 87, 8311-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc A;Reference number: A36475; MUID:91045991

A; Status: preliminary A; Molecule type: mRNA

A; Residues: 1-195, R., 197-461 < KOH>
A; Residues: 1-195, R., 197-461 < KOH>
A; Cross references: GB: M55994; GB: M38549; NID: 9339757; PIDN: AAA36755.1; PID: 9339758
A; Cross references: GB: M55994; GB: M38549; NID: 9339757; PIDN: AAA36755.1; PID: 9339758
B; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A; Accession: A48416
A; Accession: A48416
A; Accession: A48416
A; Accession: A48416
A; Residues: 23-461 < DEM>
A; Residues: Ceremoces: GB: S63368; NID: 9235648; PIDN: AAB19824.1; PID: 9235649
A; Note: sequence extracted from NID: Backbone (NCBIN: 633371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons A; Accession: A36007; MuID: 90349572
A; Accession: A36007; MuID: 90349572

A;Status: preliminary

A; Molecule type: mRNA A; Residues: 116-140, 'P', 142-195,'R', 197-362,'T', 364-461 <HEL> A; Residues: 116-140,'P', 142-195,'R', 197-362,'T', 364-461 <HEL> A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752 A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752 B; Loctscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990 A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MuID:g1056048

A;Status: preliminary A;Molecule type: protein A;Residues: 23-40;65-69;136-141;300-306 <LOE>

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tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tarkaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Accession: B38634; MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-474 < LEW>
A; Cross-references: GB: M60469; NID: g199827; PIDN: AAA39752.1; PID: g199828
R; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A; Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A; Reference number: A40254; MUID: 91246168
A; Accession: A40254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-474 <GGO>
A; Cross-references: GB: M60469; NID: g199827; PIDN: AAA39752.1; PID: g199828
A; Cross-references: GB: M60469; NID: g199827; PIDN: AAA39752.1; PID: g199828
B; Kissonerghis, M.; Fellowss, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A; Description: Characterization of the promoter region of the murine p75-TNF receptor A; Reference number: S54816
A; Accession: S54816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-22 <KISA
A;Residus: 1-22 <KISA
A;Residus: 1-22 <KISA
A;Residus: 1-22 ×RES
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Reywords: cytckine receptor; transmembrane protein
C;Reywords: cytckine receptor; transmembrane protein
C;Reywords: cytckine receptor; rensmembrane predicted <SIG>C;Reywords: cytckine receptor; receptor receptor type 2 **Status predicted <MAT>
F;1-22/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG3>
F;166-203/Domain: NGF receptor repeat homology <NG3>
F;166-203/Domain: NGF receptor repeat homology <NG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%; Score 1512; DB 2; Length 4' 63.0%; Pred. No. 1.7e-79; ive 50; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 61.3%
Best Local Similarity 63.0%
Matches 293; Conservative
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                                                                       proteins purified from human urine. Evidence
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C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; Seywords: duplication; glycoproften; receptor; transmembrane protein
C; Superfamily: tumor necrosis factor receptor; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 1-24/Domain: MGF receptor repeat homology <NG1>
F; 78 -119/Domain: NGF receptor repeat homology <NG2>
F; 120 -162/Domain: NGF receptor repeat homology <NG3>
F; 164 -201/Domain: NGF receptor repeat homology <NG3>
F; 164 -201/Domain: NGF receptor repeat homology <NG3>
F; 164 -201/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 264 -201/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 261 -279/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 261 -279/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: nGF receptor repeat homology <NG4>
F; 261 -279/Domain: nGF receptor repeat homology <NG4>
F; 262 -279/Domain: n
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                                                                                                                                                                     A.Status: preliminary
A.Status: proliminary
A.Molecule type: protein
A.Residues: 27-31 <ENG>
R.Kuhnert, P.; Kemper, O.; Wallach, D.
R.Kuhnert, P.; Semper, O.; Wallach, D.
A.Fille: Cloning, sequencing and partial functional characterization of the 5'
A.Fille: Cloning, MUID:95121934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: I38094
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule types
A;Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Blol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding
A;Reference number: A35010; WUID:90110215
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Matches 461; Conservative
                                                                                                                                               A; Accession: B35010
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417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461

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7;

Gaps

21;

Length 349; Indels

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hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Q1, J.; Utterback, T.R.; Knight, J.C.; Au Majure 36, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir A;Reference number: Z20488; MUID:94088747
A;Accession: T28623
A;Accession: T2863
A;Accession: T28623
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:X16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                             91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                       141 -GHTSVGDVICSPCGFGTYSYTVSSTDKCEP-----VPNNTFNYIDVEITLYPVNDT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
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                                                                                                                                                                                                                                                                                                         31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                         24.PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL
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A; Cross-references: RMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:g-A; Experimental source: Strain Bangladesh 1975
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                      A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                     Query Match 15.5%; Score 381.5; DB 2; Best Local Similarity 38.1%; Pred. No. 4.1e-15; Matches 80; Conservative 23; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.4%; Score 379.5; DB 2 Best Local Similarity 37.6%; Pred. No. 5.3e-15; Matches 79; Conservative 24; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 SCTRTTTGLSESILTSELTITMNHTDCNP 221
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N;Alternate names: B28R protein (COP)
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G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Deteis: 24 Nov-1999 #sequence_revision 24 Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
E;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Reference number: A72150
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                           general tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: 148854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Recession: 148854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <-RES>
A;Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
E;151-188/Domain: NGF receptor repeat homology <NGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN 193
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  59.8%; Score 1477; DB 2;
63.8%; Pred. No. 1.6e-77;
ive 47; Mismatches 108;
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Best Local Similarity 63.8%
Matches 287; Conservative
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7;

Gaps

Indels

86;

Length 348;

DB 2;

PID:9439102

9

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A; Reference number: 154182; MUID: 93252381
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310 C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology C;Superfamily: myxome virus T2 protein; NGF receptor repeat homology <NG2> F;64-105/Domain: NGF receptor repeat homology <NG3> F;106-147/Domain: NGF receptor repeat homology <NG3> F;106-147/Domain: NGF receptor repeat homology <NG3> F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: 154182
R;Beans, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. (Genomics 16, 214-218, 1993)
A;Title: Construction and evaluation of a hncDNA library of human 12p trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN--ASMDAVCTSTSPTRS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV-----CKPCAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTFSNTTSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPG-----AV 214
                                                                                                                                                                                                                                                                                                                                                 2 APVAVWAALAVGL-ELWAAA--HALPAQVAFTPYAPEPGSTCR--LREYYDQTAQMCCSK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV
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                                                                                                                                                                                                            Length 326;
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                                                                                                                                                                                                            ; Score 360.5; DB 1;
; Pred. No. 6.1e-14;
29; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 341.5; DB 2; 29.1%; Pred. No. 9.7e-13;
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ilarity 36.9%;
Conservative 29
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Best Local Similarity
Matches 75; Conserv
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Matches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overcome the host protective
                                                                                                                                                                                                                                                            A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1687, ssp. major, isolate Ind3
B;Kolykhalov, A.A.: Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library, April 1992
A;Besription: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P A;Reference number: $46868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,'
  C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAA47540.1; PID:9516449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VPNNTFNYIDVEITLYPVNDT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 PYTP-PNGKCKDIEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT----ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology F;32-66/Domain: NGF receptor repeat homology <NGF> F;68-109/Domain: NGF receptor repeat homology <NG2> F;110-151/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Tille: Wixoma virus expresses a secreted protein with homology to A.Reference number: A40566; MUID:91335768
A.Rocession: A4056
A.Molecule type: DNA
A.Rolecule type: DNA
A.Rolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-349 < KOL>
A; Cross-references: EMBL: X67117; NID: 9516428; PIDN: CAA47540...
A; Cross-references: EMBL: X67117; NID: 9516428; PIDN: CAA47540...
A; Experimental source: strain India-1967, isolate Ind3
A; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A; Title: Genes of variola and vaccinia viruses necessary to A; Reference number: S32385; MUID: 93202281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 379.5; DB 2; 37.6%; Pred. No. 5.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S32385
A; Molecule type: DNA
A; Residues: 31-168 C-825.
A; Cross-references: EMBL: X69198
A; Experimental source: strain India-1967, ssp. major
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R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, Virology 184, 370-382, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein - myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCTRITITGLSESILISELTITMNHIDCNP
                                                                             R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79; Conservative
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Matches 79; Conservat
                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
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T2 prot
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25;

215 HLPQP----VST-----RSQHTQPTPEPSTAPSTSFLL---PMGPSP-PAEGS-----

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B cell'associated surface molecule CD40, long splice form - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Accession: A46476; A46515
R; Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A; Title: Differential increase of an alternatively polyadenylated mRNA species of mur A; Reference number: A46476; MUID:92105763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A; Residues: 1-305 <TORN-
A; Cross-references: GB:MB3312; NID:g1553058
A; Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A; Note: this translation is not annotated in GenBank entry MUSCO40A, release 113.0
R; Grimaldi, J.C.; Torres, R; Rozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
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A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A;Experimental source: BALB/c, liver
                                                  A Map position: 20q12-20q13.2
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; Hosphoprotein; Surface antigen; transmembrane prot
C; Superfamily: Signal sequence #status predicted <SIG>
F; 21-207 Domain: Signal sequence #status predicted <SIG>
F; 21-193 Domain: extracellular #status predicted <SIT>
F; 194-215 Domain: transmembrane #status predicted <TMM>
F; 216-277 Domain: intracellular #status predicted <CYT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN---- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 SEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                 F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LPAQVA----FTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LPLQCVLWGCLLTAVHPEPPTACREKQYLINS--QCCSLCQPGQKLVSDCTEFTETECLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 CEDSTYTQLWNWVPEC-----LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ-----QKGTSETDTICTCEEGWHCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 PSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 277;
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C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%; Score 317.5; DB 2;
llarity 26.7%; Pred. No. 1.5e-11;
Conservative 32; Mismatches 124;
             A; Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A46515; MUID:93094586
A;Accession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 VVQQAGTNKTDVVCGPQDRLRAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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A6071.
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
B4362
T2 protein - rabbit fibroma virus
C; Species: rabbit fibroma virus, Shope fibroma virus
C; Species: rabbit fibroma virus, Shope fibroma virus
C; Species: rabbit fibroma virus, Shope fibroma virus
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C; Accession: B43692
R; Upton, C: DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A; Retenence number: A43692; MuID:87321103
A; Recension: B43692
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-325 <upra>
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-325 <upra>
A; Coss-references: GB:M17433
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F; 64-105/Domain: NGF receptor repeat homology <NG3>
F; 106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GHTRAGDTLCEKCPPHTYSDSLSPTERCGTS--FNYISVGFNLYPVN---ETSCTTTA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 PYSSNQGK-CGGHDY--EKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHA 76
                                                                                                 --TGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI----PGNASMDAVCTSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                               331 POLEPGEQSQVAHGTNGIHV-----TGGSMTITGNIYIYNGPVLGGPPGPG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 325;
                                                                                                                                                                                                                                                                                PHL-PADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.3%; Score 328; DB 2; Le
Best Local Similarity 36.9%; Pred. No. 4.3e-12;
Matches 66; Conservative 28; Mismatches 71;
                                                                                                                                                   284 HPYFPDLVQPLLPISGDVS-PVS--TGLPAAPVLEAGVPQ-
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F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                Overy Match
Best Local Similarity 25.12
Best Local Similarity 25.12
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Best Local Similarity 22.0%
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: CD30; D1S166E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-595 <DUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nerve growth factor receptor, low affinity precursor - chicken

Nathernate names: NGF receptor

C;Alternate names: NGF receptor

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: JM006; A60504

R;Large, T.H.; Weskamp, G;; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic

Neuron 2, 1123-1134, 1989
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A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
C; Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C; Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C; Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C; Superfamily: nerve growth factor receptor #status predicted <SIG>
F; 21-239/Domain: extracellular #status predicted <EXT>
F; 21-239/Domain: extracellular #status predicted <EXT>
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                                                                                                                                     14;
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A; Molecule type: mRNA
A; Residues: 1-416 < LABA
A; Experimental source: embryonic chick brain
B; Heuer J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Bev. Biol. 137, 287-394, 1990
A; Title: Structure and developmental expression of the chicken NGF receptor.
A; Reference number: A60504; MUID:90152140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340
                                                                                                                                                                                                                                                                                                                                     :| || : | | : | | : | | 326 EMLP--PAARRODPOEMEDYPGHNTAAPVOETLHGCOPVTOEDGKESRISVOEROVIDSI 283
                                                                                                                                                                                                                                                                                                                                                                                                           PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 EGOHCT --- SKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYP 163
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQ---VETQACTREQNRICTCR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 237
                                                                                                                                                                                                                                               9 ALWGCLLTAVHLGQCV------TCSDKQYLHD--GQCCDLCQPGSRLT 48
                                                                                                                                                                                          AVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AKVPHLPADK-----ARGTQGPEQQHLLITAPSSSSSSLESSASALDR-----
                                                                                                                                     Indels 115;
                                                                                   Length 305;
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F;59-100/Domain: NGF receptor repeat homology <NG2>
F;1014:139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
                                                                             ; Score 258.5; DB 2;
; Pred. No. 3.8e-08;
37; Mismatches 142;
F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 WTSCEDKNLEVLOKGTSQTNVICGLKSRMRAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ALRPPGLN----PGTAFGGDG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RAPTRNQPQAPGVEASGAG 359
                                                                                10.5%;
22.8%;
                                                                     Query Match
Best Local Similarity 22.8'
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           122
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R;Durkop, H; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A;Title: Molecular cloning and expression of a new member of the nerve growth factor A;Reference number: A42086; MUID:92154659
A;Accession: A42086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD30 antigen precursor - human N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30 C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000 C;Accession: A42086
                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                                                           S-TYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCAL 128
                                                                            Gaps
                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M83554; NID:g180095; PIDN:AAA51947.1; PID:g180096
A;Experimental source: HUT-102 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: glycoprotein; growth factor receptor; transmembrane protein F;1-18/Domain: signal sequence #status predicted <SIG> F;19-383/Domain: extracellular #status predicted <EXTS> F;384-407/Domain: transmembrane #status predicted <TMM> F;408-595/Domain: intracellular #status predicted <CTM> F;101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                     140 LRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 CTATSDAECRDLHPRWTTHTPSLAGSDS-----PEPITRDPFNTEGMATTLADIVTTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LPAQVAFTPYAPEPGS--TCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
                                                                                                                                                                                                         5 VPLLLLLLLPAGPTWGSKEKCLTKMY - - TTSGECCKACNLGEGVVQPC-GVNQTVCEPCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTSTSPT -- RSMAP-GAVHLPQPVSTRSQHTQPTPEP-----STAPSTSFLLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 GPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AVGLELWAAAHALPAQVAFTPYAPEPGSTC - · RLREYYDQTAQMCCSKCSPGQHAKVFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ALGLIFIGALRAFPQDRPFE-----DTCHGNPSHYYDKAVRRCCYRCPMGLFPTQQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 VNQ---TPSPEGEKL-----HSDSGISVDSQSLHDQQPPNQSTQGPAPKGDGS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 ADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGA 358
                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 595;
; Score 251.5; DB 1;
; Pred. No. 1.3e-07;
48; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 241; DB 2;
; Pred. No. 7.1e-07;
41; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GDB:131547; OMIM:153243
A:Map position: 1p36-1p36
C;Superfamily: NGF receptor repeat homology
      10.2%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%;
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Dp	60 QRPTDCRKQCEPDYYLDEADRCTACVTCSRDDLVEKTPCAWNSSRVCECRPGMFCST 116	Qy 228 QPTPEPSTAPSTSFLL-PMGPSPPAEGSTGDFALPVGLI
ä		
3 2	123 SNUBBOURLARFERNORFGEGVARRUIEISDDVORPCARG	
3 8	CONTROL TO THE FOREST AND THE FOREST AND THE PROPERTY OF THE PROPERTY AND	RESULT 15
<u>8</u> 5	AKPTPVSP	148/VV gene 0x40 protein - mouse N;Alternate names: 0X40 antigen
δy		C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
q	237 SGDCRKQCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAWNSSRTCECRPGMICATSATNS 296	C; Accession: 148700; 148334; S34377 R; Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
ý d	193 NASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPST 235	 Jimmunol. 131, 32017371, 1353 A,Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell A; Reference number: 148700; MUID:94044750 A. Reference number: 148700
o v	APSTSFLLPMGPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQ	A; Status: translated from GB/EMBL/DDBJ A; Molecule type: mRNA
QQ	: :	A;Residues; 1-272 <res> A;Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828 R:Rirkeland M I: *Coneland M G : Gilbert D I : Jenkins M A: Barclay A N.</res>
٥٧ ط	287 VKKRPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPT 344 1	Eur. J. Immunol. 25, 926-930, 1995 A)Title: Gene structure and chromosomal localization of the mouse homologue of rat OX a Peferance number. TAR334 MITT. 05,555413
i ò	RNOPOAPGVEASGAGEARASTGSSDSSPGG 374	A; Accession: 148334 A; Accession: translated from GB/EMBL/DDBJ
qq		A; Molecule type: DNA A; Residues: 1-14,/G', 16-272 <re2></re2>
000		A;Cross-references: EMBL:X85214; NID:g/32818; FIDN:CAA594/6.1; FID:g/32819 C;Genetics:
S12783 OX40 a	72501 14 S12781 OX40 antigen precursor - rat	A; bene: 0x40 A; Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1 C; Superfamily: CD27 antigen; NGF receptor repeat homology
N; Al	ernate names: nerve growth factor receptor homolog cies Rattus norvegious (Norway rat)	
C; AC C; AC R; Ma	ce: 30 Sept.1959 * *Sequence_revision 30 Sept.1993 *Lext_change U3-NOV-1999 * \$12783; \$12783; \$208036 * \$1.000 Sept.1999 * \$12783; \$20804 S.; Barclay, A.N.	Querry Match Best Local Similarity 27.0%; Pred. No. 3.3e-06; Matches 88; Conservative 32; Mismatches 97; Indels 109; Gaps 19;
EMBO A; T11 A; Rei	J. 9, 1063-1068, 1990 .le: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte Terence number: S12783; MUID:90214614	Qy 6 VWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAOWCCSKCSPG 60
A; AC	ession: S12783 ecule type: mRNA	Db 3 WWQQPTALLLATTGVTARRLNCVKHTYPSGHKCCRECOPG 45
A; Re: A; Crc C; Sur	idues: 1-271 <wal> ss-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831 erfamily: CD27 antigen; NGF receptor repeat homology</wal>	QY 61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRIC 118 by 46 hgwysrcdhtrdtlchpcetgfyneavnydtckQctqcnhrsgselkqnctptqdfvc 103
C; Ke; F; 1- F; 20	C;Keywords: growth factor receptor; transmembrane protein F;1-19/Domain: signal sequence #status predicted <sig> F;20-271/Product: 0X40 antigen #status predicted <mat></mat></sig>	119 TCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSS : :
F; 21.	-235/Domain: transmembrane #status predicted <tmm></tmm>	Db 104 RCRPGPGN 135
Oue Bes	Query Match 9.3%; Score 229.5; DB 2; Length 271; Best Local Similarity 27.18; Pred. No. 1.5e-06; Matchaga 70. Concernative 28. Mismatched 14.	Qy 176 TDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQ-PT 230
ογ	VWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDOTAOMCCSKCS 58	Oy 231 PEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTA-LGLLIIGVV 279
q _Q	VWVQQPTAFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQ	×
oy Db	59 PGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116	Db 232ALYLLRKAWRLPNTP 246
Qy Db	117 ICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTT 173 1 1 1 1 1 1 1 1 1 1	Search completed: February 12, 2002, 12:48:26 Job time: 148 sec
Qy	174 SSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227	

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February 12, 2002, 12:48:04 ; Search time 13.25 Seconds (without alignments) 1275.659 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                   OM protein - protein search, using sw model
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2468
1 MAPVAVWAALAVGLELWAAA......GSTEEKPLPLGVPDAGMKPS 461 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

100059 Total number of hits satisfying chosen parameters: 100059 segs, 36664827 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	home	mus m	P34015 variola vir	P29825 myxoma viru		shope		шns п	Q92956 homo sapien	mus n	P18519 gallus gall	Q28203 bos taurus	P28908 homo sapien	P15725 rattus norv	P47741 mus musculu	homo	P08138 homo sapien	pos t	P50555 sus scrofa	P20334 mus musculu	ratt	P25118 mus musculu	rattu	homo	P19438 homo sapien		P51867 bos taurus			. P92127 giardia lam	P48960 homo sapien	077736 sus scrofa	Q63199 rattus norv
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| Nature 398:533-538(1999).
| Contain Inger 2: 1.5 | Nature 398:533-538(1999).
| Contain Inger 2: 1.5 | Nature 398:533-538(1999).
| Contain Inger 3: 1.5 | Nature 398:533-538(1999).
| Contain Inger 3: 1.5 | Nature 3: 1.5 | 
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                                                                                                                                                                                                                                                                         Construction of the MEDINE-31010 of ligand binding, internalization, and receptor observed by the model of ligand binding of ligand binding, internalization, and receptor observed binding.
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Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
"Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX
                          Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
                                                                                                    "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
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MEDLINE=91056048; PubMed=2173696
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ProDom; PD000771; TNFR_c6; 1.
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US2161; AACS0622.1; JG
US2162; AACS0622.1; JG
US2163; AACS0622.1; JG
US2164; AAAS0622.1; JG
MS5994; AAA36755.1;
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PIR, A36007; A36007.
PIR, A36475, A36475.
PIR, B35010; B35010.
PIR; A23666; A23666.
PDB; ICA9; 12-APR-99.
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                                       TUMOR NECROSIS FACTOR RECEPTOR
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                                                       EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                         Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                              MEDLINE=91246168; PubMed=1645445; Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                              tumor
                                                                                        MEDLINE-91187885; PubMed-1849278; Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Nong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumon necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (INF-R2) (P75).
INFRSF1B OR TNFR2 OR INFR-2.
                                                                                                                                                                                                                                                                                                   Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWER-CYS 2.
TWER-CYS 3.
TWER-CYS 4.
TWER-CYS 4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1314883; Tnfrsflb.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M59378; AAA40463.1; -. U39488; AAA85021.1; -. X87128; CAA60618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M60469; AAA39752.1; -.
                                                                                                                                                                                                                                                                              SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-22 FROM N.A.
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2588
2588
203
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203
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68
68
68
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HSSP; P19438; INCF.
                        Mus musculus (Mouse)
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                        STRAIN-NOD;
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TRANSMEM
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EMBL;
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STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE-932025281; PubMed-834129;
Shchelkunow S.N., Blinow V.M., Sandakhchiew L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356
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                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-!- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP
                                                                                                                                                                                                                                                                                                                          120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
8
                                                                                                                                                                                                                    Length 474
                                                                                                                                                                                                                                         Pred. No. 4.2e-81;
50; Mismatches 114; Indels
                                                                                                                                                              462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS
                                                                                                                                                                                                                      61.3%; Score 1512; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                50319 MW;
                                                                                                                                                                                                                                         63.0%;
                                                                                                                                                                                                                                         Best Local Similarity 63.0
Matches 293; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN C22/B28 HOMOLOG.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT----ST 203
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIVOLOGY 184:370-382(1991).

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS THE TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL REPECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91335768; Pubmed-1651597; Upton C., Macen J.L., Schreiber M., McFadden G.; Myxoma virus expresses a secreted protein with homology to the necrosis factor receptor gene family that contributes to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-ATR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                  108 2 X TNFR-CYS.
66 TNFR-CYS 1.
108 TNFR-CYS 2.
38189 MW; D45D40B5C6E780EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 15.4%; Score 379.5; DB 1; Best Local Similarity 37.6%; Pred. No. 1.2e-15; Matches 79; Conservative 24; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPIRSMAPGAVH -- LPQPVSTRSQHTQPTP 231
                                                                                                                                                                                                                                                       PS00652; TNFR_NGFR_1; 2. PS50050; TNFR_NGFR_2; 2.
                                                                                                 EMBL, X69198; CAA49137.1; -.
EMBL, X67117; CAA47540.1; -.
PIR, D36858, D36858.
PIR, S35907; S35907.
PIR, S46888; S46888.
HSSP; P19438; INCF.
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                     108
66
108
                                                                                                                                                                                                                                                                                                                                                 349 AA;
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NCBI_TaxID=31530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VT2_MYXVL
P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virulence.
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DOMAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                        | December | Production | Program | Production | Program | Production | Production | Program | Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN--ASMDAVCTSTSPTRS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
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01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
LYMPHOTOXIN) (TUMOR NECROSIS FACTOR CEPTOR
LIBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.; "Construction and evaluation of a hncDNA library of human 12p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.6%; Score 360.5; DB 1; Length 326; Best Local Similarity 36.9%; Pred. No. 1.4e-14; Matches 75; Conservative 29; Mismatches 86; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 MAPGAVHLPQPVSTRSQHTQPTP 231
                                                                                                                                                                                                                                   EMBL; M95181; AAA46632.1; EMBL; A23729; CAA01688.1; -. PIR; A40566; GOVZML. HSSP, P19438; 1TNR. InterPro; IPR001368; TNFR_C6. Pfam; PP00020; TNFR_C6; 2. ProDom; PD000771; TNFR_C6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GPNEVVKTSEFSVTLNHTDCDP
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SEQUENCE FROM N.A.
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TNRC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCR----PCDPVMGLEEIAPCTS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV-----CKPCAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 APVAVWAALAVGL-ELWAAA--HALPAQVAFTPYAPEPGSTCR--LREYYDQTAQMCCSK '56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 APGLAWGPLVLGLFGLLAASOPOAVP-----PYASE-NOTCRDQEKEYYEPQHRICCSR 61
                                                                                                                   -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IMMUNE DEVELOPMENT.
                                                                                                                                              -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                              Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
"A lymphotoxin-beta-specific receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..) (POTENTIAL)...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 435;
transcribed sequences derived from a somatic cell hybrid.";
Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624626E6022F656F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 341.5; DB 1 29.1%; Pred. No. 2.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 X TWFR-CYS.
TWFR-CYS 1.
TWFR-CYS 2.
TWFR-CYS 4.
BY SIMILARITY.
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                                                      PubMed-8171323;
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
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Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
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                                                                                                       Science 264:707-710(1994).
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177
435 AA;
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                                                    MEDLINE-94225209;
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MIM; 600979
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Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91207415; PubMed=1850261; Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C., McFadden G., Goodwin R.G.; McFadden G., Goodwin R.G.; T. Copen reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor.; Blochem. Blophys. Res. Commun. 176:335-342(1991).

-: FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO TREACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL RANITUREL EFFECTS OF THE CYTOKINE.

-: SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-87321103; PubMed-2820128;
Upton C., Delange A.M., McFadden G.;
"Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome.";
Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                               -----TGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
                                                                                                                                                                                                                                                                                                                                         284 HPYFPDLVQPLLPISGDVS-PVS--TGLPAAPVLEAGVPQ-----QQSPLDLTRE--- 330
167 GTFSNTTSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPG------AV 214
                                                                     173 GHFQNTSSPSARCQPHTRCENOGLVEAAPGTAQSDTTC--KNPLEPLPPEMSGTMLMLAV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                             231 LLPLAFFLLLATVFSCIWKS-----HPSLCRKLGSLLKRRPQGEGPNPVAGSWEPPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLEPGEOSOVAHGTNGIHV-----TGGSMTITGNIYIYNGPVLGGPPGPG 376
                                                                                                                                                                                                                                                                                                                                                                                                                             301 PHL-PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
17-MOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
                                                                                                                                           215 HLPQP----VST-----RSQHTQPTPEPSTAPSTSFLL---PMGPSP-PAEGS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shope fibroma virus (strain Kasza) (SFV)
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EMBL; A23727; CAA01687.1; -.
PIR; B43692; B43692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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P25943;
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Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Natismith J.H., Thomas D.;
The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
Protein Sci. 7:1124-1135(1998)
Protein Sci. 7:1124-1135(1998)
I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
I- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
I- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
WWWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                  PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CEL. SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
                                                                                                                                                               13.3%; Score 328; DB 1; Length 325; 36.9%; Pred. No. 1.1e-12; ive 28; Mismatches 71; Indels 14; Gaps
                                                                                                                                                                                                                                                   PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                 151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI----PGNASMDAVCTSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  model
                                                                (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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MEDIATE-97189482; Pubbed-9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional methor ligand binding domain of the human B cell receptor CD40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-89356608; PubMed-2475341;
Stamenkovic I., Clark E.A., Seed B.;
"A B-lymphocyte activation molecule related to the nerve of factor receptor and induced by cytokines in carcinomas.";
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. ..) (POTINELNEED (GLCNAC. ..) (POTINE
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                                                                                                                   MW.
                                                                                                                   35132
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                                                                                                                                                                                                  Conservative
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 104
1186
1105
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205
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 63
105
148
105
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205
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325 AA;
                                                                                                                                                                                 Similarity 66; Conserv
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P25942:
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CARBOHYD
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEDSTYTQLWNWVPEC-----LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPAQVA----FIPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 PSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TNKAPHPKQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN----
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                             Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                               CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC, . .) (PC
BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 VVQQAGTNKTDVVCGPQDRLRAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 ----LPAD-KARGTQGPEQQHLLITAPSSSSSSLESSASALDRR 341
                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.9%; Score 317.5; DB 1; Best Local Similarity 26.7%; Pred. No. 3.8e-12; Matches 92; Conservative 32; Mismatches 124;
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                       POTENTIAL
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                                                                                              InterPro: IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
Probom; P000071; TNFR_c6; 1.
SMARI: SMO008; TNFR; 4.
PROSITE; PS00652; TNFR, NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
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Μ.
                                                      EMBL; X60592; CAA43045.1; -.
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277 AA;
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ID TNRC_MOUSE
AC P50284;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human secreted pro	Amino acid sequenc	Linking B region #	Sequence of a pept	Camel Iq 2-heavy c	Peptide encoded by	Peptide #5770 enco	Peptide #6169 enco	Amphotropic hyperv	Human INTERCEPT 21	Human ORFX ORF2454
SUMMARIES	ID	AAB56300	AAW59911	AAR15261	AAR49722	AAR49536	AAY01285	AAM19336	AAM32132	AAW88522	AAB61193	AAB42690
	DB	21	19	12	15	15	20	22	22	20	22	21
	Query Match Length DB ID	47	49	45	54	54	41	47	47	46	52	55
o#	Query	22.7	22.4	19.5	19.2	19.2	18.7	18.5	18.5	18.2	18.2	18.0
	Score	68.5	67.5	59	28	58	56.5	98	26	52	55	54.5
	Result No.	Н	7	m	4	S	9	7	8	6	10	11

Sequence of human Human 5' EST relat Peptide #4543 enco Peptide #4567 enco Peptide #7067 enco Peptide #5529 enco Peptide #5529 enco Peptide #669 enco Peptide #665 enco IgA protease specification in the Human 1941 hinge region profuman 1941 clared profuman secreted profuman secreted profuman secreted profuman mucin peptid Linking B region #640 enco Portio Sequence of hinge Cancinoma-associat Peptide encoded by Fragment of human Lck binding active	ALIGNMENTS AAB56300 standard; Protein; 47 AA. AAB56300; 13-MAR-2001 (first entry) Human secreted protein sequence encoded by gene 99 SEQ ID NO:394. Human secreted protein; diagnosis; immunosuppressive; antiarthritic; antiprollerative; cytostatic; cardiant: vasotropic; cerebroprorective; antipacterial; virucide; fungicide; ophthalmolgical; gene therapy; pathological condition; autoimmune disease; rheumatoid arthritis; hyperprollerative disorder; acerebrovascular disorder; andiogenesis; nervous system disorder; cerebrovascular disorder; cerebrovascular disorder; cerebrovascular disorder; corneal infection; Alzheimer's disease; infection; ocular disorder; corneal infection; Mox00070042-A1. 23-NOV-2000. 11-MAY-2000; 2000WO-US12788. 13-MAY-1999; 99US-0134068. (HUMA-) HUMAN GENOME SCI INC. Kosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE; Duan RD, Florence KA, Soppet DR;
AAP81606 AAM17997 AAM17997 AAM17992 AAM350661 AAW35739 AAW35739 AAW35739 AAW35739 AAW35739 AAW3666 AAW3696 AAW3696 AAW36996 AAW36996 AAW36996 AAW42923 AAW64623 AAW64623 AAW64623 AAW64623 AAW65002 AAW65002 AAW66002 AAW6002 AA	. ALIGNMENT ; 47 AA. uence encoded lagnosis; immu rative; cytost li; gene therap toid arthritis lsorder; card anglogenesis, tion; ocular d food additive food additive 8. 8. 8. 8.
22000000000000000000000000000000000000	first entry) first entry) protein sequence d protein; diagnos antiproliferative ive; nootropic; ne thalmological; ger ease; rheumatoid a iovascular disorder i disorder; anglog sease; infection; skin aging; food skin aging; food genome SCI INC. en SM, Moore PA, ence KA, Soppet I
	standard; P i 001 (first creted prote ecreted prote matic; antip rote(170; n e; ophthalm, n e; ophthalm of ne disease; ascular diso r's disease; aling; skin iens. 042-A1. 000; 2000WO- 999; 99US- HUMAN GENOME ' Ruben SM, Florence K
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	T 1 300 AAB56300 st. AAB56300; 13-MAR-2001 Human secre Hundicide; cantirheumat cant
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of plague and bacteria on teeth
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                                                                                                                                                                                  The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB5607 to AAB56362. Human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropt; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The human secreted polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are dispansed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The proteins can also be used to ald wound healing and epithelial cell proliferation, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 food additive or preservative to increase or decrease storage capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proteins can also be used
                                                                     Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene encoding a mutanase enzyme - used for prevention and removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   box; alpha-1,3 glucoside bond; mutan; plaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSTRSQHTQPTPE----PSTAPSTSFLLPMGPSPPAEGST 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the mutanase enzyme PT box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68.5; DB
Pred. No. 3.1;
3; Mismatches
                                                                                                                                        Disclosure; Page 1035; 1065pp; English.
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Best Local Similarity 40.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutanase enzyme; PT
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                                           This is the amino acid sequence of the mutanase enzyme PT box, which decomposes the alpha-1,3 glucoside bond of mutan. The mutanase enzyme is used in the method of the invention for prevention and removal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fungal (hemi)cellulose degrading enzymes - for prodn. of lig. fuel gas and feed protein, have specified carbohydrate binding domain
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and/or Thr and/or Gln. It can be incorporated in a fusion protein comprising a catalytic domain from a cellulase, e.g. a Bacillus endoglucanase, and a carbohydrate binding domain from a fungal endoglucanase. See also AAR15254-R15260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a cellulose- or hemicellulose-degrading enzyme and which are enriched in the amino acids Gly and/or Asn and/or Pro and/or Ser
                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                    Length 49;
                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 12; Length 45;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                1 TST-SPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP
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                                                                                                                                                                                                                                    DB 19;
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                                                                                                                                                                                                                                  Score 67.5;
Pred. No. 4;
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37.8%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 46; 73pp; English.
Claim 2; Page 5; 15pp; Japanese.
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR15261 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBD; hemicellulosic substrate;
Trichoderma reesei; cellulase;
                                                                                                                                                                                                                                    22.4%;
35.3%;
                                                                                                                  plague and bacteria on teeth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-DK00124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Woldike HF, Hagen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-353766/48.
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09117244-A.
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Camelus dromadarius.
                                                                                                                                              21-AUG-1992;
                                                                                                                                                                                                                 Casterman C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09903978-A1
                                                                                                                                                                  21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1998;
                                                                                                                            02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-1999
                                                                                                         EP584421-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY01285;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                     (CAST/)
                                                                                                                                                                                              (HAME/)
                                                           Region
                                                                               Region
                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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                                                                            Sequence of a peptide which is part of the heavy (H) chain (CH3) of an
                                                                                                                                                                                                                                                                                                                                                  A novel immunoglobulin (Ig) is claimed which comprises two heavy (H) polypeptide chains sufficient for the formation of a complete antigen binding site or several such chains. The Ig is devoid of light (L) polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E. coli, by: cloning a DNA or cDNA sequence coding for the VH domain of an Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids; recovering the cloned fragment after amplification using a 5' primer contg. an Xho site and a 3' primer contg. the Ses site having the sequence in AAQ44383; cloning the recovered fragment is a vector; transforming host cells; and recovering the expression product of the VHH coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; Ig; heavy chain; constant region; variable region; antibody engineering; IgG2; IgG3.
                                                                                                                                                                                                                                                                                                     Immunoglobulins devoid of light chains - also processes for their preparation, and protein and nucleotide sequence encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide encoding the peptides in AAR49721-24 is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camel Ig 2-heavy chain molecule (clone no. 72/79).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58;
Pred. No.
                                                                                                          chain; Camelid
                      54 AA.
                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 65; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.2%;
31.6%;
                    AAR49722 standard; peptide;
                                                                                                                                                                                   93WO-EP02214
                                                                                                                                                                                                      92EP-0402326
93EP-0401310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR49536 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 31.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                Casterman C, Hamers R;
                                                                                                       Immunoglobulin; heavy
                                                                                       immunoglobulin (Ig).
                                                                                                                                                                                                                                    CASTERMAN C.
                                                                                                                                                                                                                                                                                   WPI; 1994-083195/10.
                                                                                                                            Camelus dromedarius
                                                                                                                                                                                                                                   (CAST/) CASTERMAN
(HAME/) HAMERS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AA;
                                                                                                                                                                                   18-AUG-1993;
                                                                                                                                                                                                      21-AUG-1992;
21-MAY-1993;
                                                          22-AUG-1994
                                                                                                                                              WO9404678-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-1994
                                                                                                                                                                 03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                       AAR49722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR49536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
RESULT * 4
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Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein; RPRP; arabino-galactan protein; AGP; glycopeptide; internal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This 2-chain Ig molecule lacks any light chains. The Ig has e.g. improved solubility and aggregate much less than heavy chains of 4-chain 19s. The Igs can be used normally for e.g. diagnosis, therapy, in vaccines, for isolation and purification of antigens and in the production of anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated immunoglobulin molecules devoid of light polypeptide chains - consisting of heavy polypeptide chains only, obtd. from Camelid serum, for use as antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                            "heavy chain variable region"
                                                                                                                                             "heavy chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ipgpgpkpgpgpgpkpgpkpepectcpkcpapellg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 1
Pred. No. 38;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide encoded by HRGP gene cassette.
                       6..40
/note= "hinge region"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.2%;
31.6%;
                                                                                                                                                                                                                                                                                                                                               92EP-0402326.
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                                                                                                                                                                                                                                                                                              92EP-0402326
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Best Local Similarity 31.6
Matches 12; Conservative
                                                                                                                      41..54
/note=
                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                                                CASTERMAN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-067061/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       HAMERS
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analyzing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53.
                                                                                                                                                   47 AA;
                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                      genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                         WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
                                                                                                                                                                                                                                                                                                      AAM32132;
                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                       cervical
                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                             Probe;
                                                                                                                                                                                                                                                                          AAM32132
                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                               The invention relates to novel synthetic genes for plant gums. A new approach is described to the production of hydroxyproline-rich glycoproteins (RRGPS), repetitive proline-rich proteins (RPBPS) and arabino-galactan proteins (AGPS). Synthetic genes comprising a nucleic acid encoding the peptide (AAY01267) can be engineered for the production of repetitive glycopeptide modules in calls. The invention provided a new approach to the problem of producing plant gums that is not dependent on environmental factors and greatly simplifies the production of a variety of naturally occurring gums as well as designer
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #5770 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                    Gaps
                                                                                    οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                               human; microarray; gene expression; cervical epithelial cell;
                                                                                   Novel synthetic gene designed from repetitive peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gelome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                    ж
Э
                                                                                                                                                                                                                                                                 Length 41;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                               18.7%; Score 56.5; E
43.3%; Pred. No. 40;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                       strasppppspppps---ppppspp 30
                                                                                                                                                                                                                                                                                                      21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
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                                                                                                              Disclosure; Fig 1; 72pp; English
                                                                                              hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                     AAM19336 standard; Protein; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0207456.
2000US-0608408.
2000US-052366.
2000US-0234687.
2000US-0234587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
97US-0897556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                    Conservative
                                                      WPI; 1999-132225/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53
                                                                                                                                                                                                                                                                          Local Similarity
                   (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                     41 AA;
                                                                N-PSDB; AAX27690
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer
                                    Kielszewski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
21-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                       AAM19336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perm SG,
                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                           AAM19336
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The present invention relates to human single exon nucleic acid probes (SENN: see AAIIO068-AAI20459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                         measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #6169 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST-SFLLPMGPSPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pctvaappaaaap---peragptspspaavaapstlssscpatpcpp 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Claim 27; SEQ ID No 24162; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000us-0180312.
2000us-0207456.
2000us-0608408.
2000us-023366.
2000us-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.5%;
38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.5
Best Local Similarity 38.3
Matches 18; Conservative
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Human; INTERCEPT 217; INTERCEPT 297; TANGO 276; TANGO 292; TANGO 325; TANGO 331; TANGO 331; TANGO 331; TANGO 332; Cytostatic; antiinflammatory; antiarrhythmic; antipsociatic; gene therapy; cancer; inflammatory disorder; cardiac disorder; arrhythmia; skin disorder; psorlasis.
                                                                                                                                                                                                                                                                                                                                                                Isolated human proteins are used for diagnosis, treatment and prevention of cancers, inflammatory disorders, cardiac disorders e.g. arrhythmia, and skin disorders e.g. psoriasis -
                                                                         Human INTERCEPT 217 cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 297; 372pp; English.
 standard; Protein; 52 AA.
                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                        16-JUN-2000; 2000WO-US16658.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                 Holtzman DA,
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-061966/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AA
                                                                                                                                                                                       WO200100638-A2.
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                29-JUN-1999;
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                                                  03-APR-2001
                                                                                                                                                                                                               04-JAN-2001.
                                                                                                                                                                                                                                                                                                                 Kirst SJ,
                         AAB61193;
 AAB61193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a retroviral vector particle (RVPI), having a modified retroviral envelope polypeptide which includes the having a modified retroviral envelope polypeptide which includes the protein or peptide. Retroviral vectors made targetable by modification of the HP region enable the delivery of desired genes to a variety of cell types. Unlike prior art modifications in the receptor binding region, the particle does not disrupt envelope structure to impair folding, processing, and incorporation of the envelope protein. The present sequence represents an amphotropic hypervariable polyproline region truncated peptide from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                      Gaps
                                                                                                                                                                                                                                                                           Amphotropic hypervariable polyproline region truncated peptide N-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New retroviral vector particle - has envelope polypeptide modified in the hypervariable polyproline region to enable cell targeting
                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
;
                                                                                                                                                                                                                                                                                                    Hypervariable polyproline region; amphotropic gp70 protein; human cytomegalovirus; hCMV; retrovirus; envelope protein.
                                                               Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20; Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                             5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST-SFLLPMGPSPP 50
                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 2
Pred. No. 52;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 64;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55;
                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New retroviral vector particle
                                                                                                                                                                                                 AAW88522 standard; peptide; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%;
                                                            Query Match
Best Local Similarity 38.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US09718
                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0856074
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.2
Best Local Similarity 40.5
Matches 15; Conservative
human genetic disorders.
                                                                                                                                                                                                                                                                                                                                          Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059696/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 AA;
                        47
                                                                                                                                                                                                                                                                                                                                                                 WO9851700-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson WF,
                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1998.
                                                                                                                                                                                                                                                   12-MAR-1999
                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                          AAW88522;
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                                                                                                                                                                                       AAW88522
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SXCC
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Barnes TS;

Sharp JD,

Fraser CC,

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The present sequence is given in a specification relating to isolated human proteins designated INTERCEPT 217, INTERCEPT 297, TANGO 226.

TANGO 292, TANGO 331 and TANGO 332. These proteins are useful as modulating agents or as targeting agents for developing agents to regulate cellular processes e.g. growth, proliferation, survival, differentiation and activity of human tissues. Diseases which can be diagnosed, prevented and treated by administration of these polypeptides, their nucleic acids and modulators include cancers, inflammatory disorders, cardiac disorders e.g. arrhythmia, and skin disorders e.g. cardiac disorders e.g. arrhythmia, and skin disorders e.g. arrhythmia, and skin disorders e.g. arrhythmia, and skin disorders e.g. arrhythmia.

Comparises molecules or ribozymes can be used to inhibit expression and in target cells. Fragments of the nucleic acid molecules encoding the isolated proteins are used as hybridisation probes and as colymerase chain reaction (PCR) primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2454 polypeptide sequence SEQ ID NO:4908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 22;
Pred. No. 72;
5; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 PVSTRSQHTQPTP--EPSTAPSTSFLLPMGPSPPAEGST
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Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.9
Matches 14; Conservative
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RESULT 10 AAB61193

Human Cu/Zn superoxidedismutase polymer; pSODCF1SODHA1; human immunoglobulin A1; hinge region; antiinflammatory agent;

Location/Qualifiers

Homo sapiens

1..20 /note="Hinge #1"

4..20 /note="IgA1"

Protein Region

88EP-0302244 87US-0026143

15-MAR-1988; 16-MAR-1987;

21-SEP-1988 EP283244-A.

(CHIR-) CHIRON CORP.

Sequence of human immunoglobulin Al (IgAl).

02-OCT-1990 (first entry)

AAP81606;

AAP81606 standard; protein; 21 AA.

RESULT 12 AAP81606

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; nearcoprotective; anticorvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; whypotensive; dermatological; immunosuppressive; antidiabetic; hypoteric; antidiabetic; wardiabetic; hypoterical disease; neurodegenerative disorder; proliferative disorder; hypoterical disease; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aphastic anaemia; nocturnal haemoglobinuria; burn; wound; hone damage; cartilage damage; antiinflammatory disease; coagulation; whrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vascing antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithroid; and antiamemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The
                                                      nootropic; neuroprotective; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, prollferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 4083; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC76899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000.
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            WANTE STATE OF STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SOD monomer - IgA - SOD monomer)x or (SOD monomer - IgA - SOD monomer - IgA - SOD monomer - IgA - SOD monomer)x - a 10-100 amino acid long segment of an immunoglobulin hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Cu/Zn superoxide dismutase (SOD) polymer of SOD units of at least 2 SOD monomers covalently coupled, carboxy terminus to amino terminus, to each other by a polypeptide spacer of at least 3 amino acids is claimed. The polymers are of formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN80435 was used to make pSODCFISODHA1 encoding bacterial expression spacer-linked human SOD monomers. AAN80435 encodes human IgA1 hinge region beginning at AA residue 226 to avoid the Cys 225 residue with BamHI and NocI sites at its ends. The SOD polymers have an extended circulatory life and retain the activity of SOD. The cloning and sequencing of human SOD (hSOD) cDNA and prodn. of hSOD in bacteria and yeast are described in EP-138111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superoxidedismutase polymers having extended in vivo life - comprising superoxidedismutase monomers covalently coupled by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 9; Length 21;
Pred. No. 36;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 LPQPVSTRSQHTQPTPEPSTAPSTS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||| : | ||| ||| |: |
1 iaqpvps----tpptpspstpptps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    Hallewell RA, Mullenbach G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-265657/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide spacers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAN80435
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RESULT

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Gaps

11;

19 PVSTRSQHTQPTPEPS-----TAPSTSFLLPMGPS---PPAEGSTG 56

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DB 21; Length 55;

18.0%; Score 54.5; D 38.3%; Pred. No. 85; Live 1; Mismatches

Conservative

Query Match Best Local Similarity Mat£hes 18; Conserv

AAY65289

AAY65286

Homo

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(SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs are be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #4543 encoded by probe for measuring placental gene expression.
                                                                                                                                           Peptide #4431 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                   Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful f
analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 10; Indels
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Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 22823; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0608408
                                                                                  (first entry)
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 AA;
                                                                                                                                                                                                                                    cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer.
                                                                                                                                                                                                                                                                                                                                              WO200157278-A2.
                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                  12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
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                          AAM17997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences, corresponding to human secreted proteins. AAY64631 to AAX45438 represent the EST-related proteins corresponding to AAX42265 to AAX43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in game expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used to accompanie to the products of the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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Pred. No. 62;
2; Mismatches 8; Indels
                                                                                                                                                                                             Human 5' EST related polypeptide SEQ ID NO:1450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A, Giordano J;
                       AAY65289 standard; Protein; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 PTPEPSTAPSTSFLLPMGP--SPP 50
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Best Local Similarity 50.0%;
Matches 12; Conservative
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98US-0069047.
                                                                                                                                        (first entry)
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N-PSDB; AAZ42903.
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genetic disorder

AAM17997 standard; Protein; 50 AA.

RESULT 14

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AAM17997 ID AAM1

Sequence

Length 50;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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40.0%; Pred. No. 87;
tive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID No 30775; 654pp; English.
                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                            04-FEB-2000, 2000US-0180312.
26-MAY-22000, 2000US-0207456.
30-UJN-22000, 2000US-0632366.
03-AUG-2000, 2000US-0632366.
21-SEP-22000, 2000US-0234687.
27-SEP-2000, 2000US-0234687.
                                                                                                 30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0°
Matches 10; Conservative
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                                          WO200157272-A2.
              Homo sapiens.
                                                                       09-AUG-2001
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Search completed: February 12, 2002, 12:59:58 Job time: 193 sec

27 TQPTPEPSTAPSTSFLLPMGPSPPA 51 tiplpppasstppmlplplppspps 41

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20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last ann
TUMOR NECROSIS FACTOR RECEPTOR
  44956 MW;
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                                                       119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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  415 AA;
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                                               Similarity
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Q92956; Q9UM65;
  SEQUENCE
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Best Local
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                                                         Matches
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                                                                                                                                                                                                                                                                                             -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
                                                                                                                       STRAIN-CVB; TISSUE-Lung;
MEDIZIRE-96072804; PubMed-7594541;
Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
Browning J.L., Ware C.F.,
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
and expression.";
J. Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                                                                           'The murine lymphotoxin-beta receptor cDNA: isolation by the signal
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                    IMMUNE DEVELOPMENT.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                          MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
101-NOV-1997 (Rel. 35, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
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                                                                                                                                                                                                                                                                   sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS 2.
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ProDom; PD000771; TWRR_c6; 1.
AMART; SM00208; TWRR; 3.
PROSITE; PS00652; TWRR_WGFR_1; 2.
PROSITE; PS50060; TWRR_WGFR_2; 3.
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                                                        Mus musculus (Mouse)
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                             SEQUENCE FROM N.A
                                                                                        NCBI_TaxID=10090;
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                                              LTBR OR TNFCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TQVKK------KPLCLQREAKVPHLP------ADKARGTQGPEQQHLLIT 322
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                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 TSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPIRSMAPGAVHLPQPVSTRSQHTQ 228
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                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                              7 WAALAVGLELWAAAHALPAQVAFTPYAPEPGSTC--RLREYYDQTAQMCCSKCSPGQHAK 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 CIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPF--SKEECAFRSQLETP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 VTGNIYIYN------GPVLGGT-RGPGDPPAPPEPPYPTPEEGAPGPSELSTP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Last sequence update)
C-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR
(HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE
                                                                                                                                                                                                                                                                                                                           14 WGPLLLGLSGLLVA-SQPQLV--PPYRIE-NQTCWDQDKEYYEPMHDVCCSRCPPGEFVF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97306336; PubMed=9162061;
Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C., Porter T.G., Truneh A., Young P.R.;
"A newly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in Jymphocyte activation."
J. Biol. Chem. 272:14272-14276(1997).
                                                                                                          12.8%; Score 317; DB 1; Length 415; 24.9%; Pred. No. 6e-12; ive 50; Mismatches 166; Indels 142;
29B326A566AEF661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AA
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                                          Zhang W., Wan T., Cao X.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR TNESF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
-- PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED.
THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144

    145 PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS 204

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNER-CYS 1.

TNER-CYS 2.

TNER-CYS 3.

BY SIMILARITY.

BY SIMI
                                                                                                                                                                                                                                            IN LUNG, SPLEEN, AND THYMUS.
SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46CE13C2C70242C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 259; DB 1; 32.8%; Pred. No. 9.4e-09; Live 23; Mismatches 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U70321; AAB58354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF153978; AAF75588.1;
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
1119
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162
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93
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[3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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DOMAIN
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DISULFID
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REPEAT
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REPEAT
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                                                           el. 23, Created)
al. 34, Last sequence update)
el. 38, Last annotation update)
PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).

-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SUBCELLULAR: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUFR-CYS 2.
TUFR-CYS 3.
TUFR-CYS 3.
N-LINED (GLCNAC. . .) (POTENTIAL).
C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-92105763; PubMed-1370315; Driess R.M., Clark E.A.; Torress R.M., Clark E.A.; "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."; J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodom; PD000771; TNFR.c6; 1.
SMART; SM00208; TNFR, 4.
PROSITE; PS00652; TNFR.NGFR_1; 1.
PROSITE; PS0050; TNFR.NGFR_2; 4.
Receptor; B-call; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                             289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD40L RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C; TISSUE-Liver; MEDLINE-93094586; Pubmed-1281194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M94126; AAA37404.1; -.
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M94127; AAA37404.1; JOINED PIR; A46476; A46476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 N
32111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M83312; AAB08705.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00020; TNFR_c6; 4
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P25942; 1CDF.
MGD; MGI:88336; Infrsf5.
                                                                                       15-JUL-1999 (Rel. 38,
                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153
289 AA;
                                                           (Rel.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
20
194
                                                                                                                       TNFRSF5 OR CD40
                                                                                                      CD40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C;
Torres R.M.;
                                                           01-AUG-1992
01-OCT-1996
                             CD40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro:
                                                                                                                                                                                                                                                                                                                   REVISIONS
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REPEAT
CARBOHYD
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TRANSMEM
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REPEAT
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RESULT 10
CD40_MOUSE
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REPEAT
                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHCTALEKTQCHPCDSGEFSAQWNREIRCHQ-HRHCEPNQGLRVKKEG-TAESDTVCTCK 106
                                                                                                                                                                                                                                                                  225
                                                                                                                                                                PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRP 181
                                                                                                                                                                                                                                            297
                                          Gaps
                                                                                                         55 VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQ---VETQACTREQNRICTCR 121
                                                                                                                                                                                               182 HQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                               64
                                                                                    9 ALWGCLLTAVHLGQCV------TCSDKQYLHD--GQCCDLCQPGSRLT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P., Shooter E.M., Reichardt L.F.; Shooter E.M., Reichardt L.F.; Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system."; Neuron 2:1123-1134 (1989).
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PTM: N- AND O-GELYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
-!- SIMILARITY: COWTAINS A LA.NGER/TNER-TYPE CYSTEINE-RICH REGION.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                 ------YIKKVVKKP---KDN
                                                              AVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAK
                                                                                                                                                                                                                                           STSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE
                                                                                                                                                                                                                                                                                      341
                                                                                                                                                                                                                                                                                                           226 EMLP -- PAARRODPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
                                          Indels 103;
                   Length 289;
                                                                                                                                                                                                                                                                                      298 AKVPHLPADK ------ARGTQGPEQQHLLITAPSSSSSLESSASALDRR
                   ; Score 252.5; DB 1;
; Pred. No. 2.3e-08;
38; Mismatches 134;
                                                                                                                                                                                                                    164 WTSCEDKNLEVLQKGTSQTNVICGLKSRMRAL-----
                                                                                                                                                                                                                                                                                                                                                                    416 AA
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90166579; PubMed-2560385;
                   10.2%;
22.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000488; Death.
               Query Match
Best Local Similarity 22.55
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (GP80-LNGFR) (P75 ICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JN0006; JN0006.
PIR; A60504; A60504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                  NGFR_CHICK
P18519;
                                                                                                                               49
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81 S-TYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAP 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 LRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 GSSQPVVSRGTADNLIPVYCSI----LAAVVVGLVAYIAF---KRWNSCKONKOGANNRP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LPAQVAFTPYAPEPGS--TCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 CTATSDAECRDLHPRWTTHTPSLAGSDS-----PEPITRDPFNTEGMATTLADIVTTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                          LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
                                                                                                                                                                                                                                        Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
C-Y (IN REF. 2).
T-> K (IN REF. 2).
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25.1%; Pred. No. 3.7e-08;
tive 48; Mismatches 164
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TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 3. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44654 MW;
Interpro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
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173
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396
416 AA;
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Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
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16;

us-09-800-909-2.rsp

VVAIPGNASMDAVCTSTSPTRSM 209 173 VEQHVGTNKTDVVCGFQSRMRTL 195

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEG-----TLNTDTICVCVEGQHCT--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 SHTCESCTPHSLCLPGFGVKQ1ATGLLDTVCEPCPLGFFSNVSSAPEKCHRWTSCERKGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 CEDSTYTQLWNWVPEC-----LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN---- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPLQCLFWGFFLTAVHSEPATACGEKQY - - PVNSLCCDLCPPGQKLVNDCTEVSKTECQS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LPAQVAF----TPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS 77
                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT)
TNFRSF5 OR CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                MEDLINE=97281252; PubMed=9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
RECEPLOR: B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 19 POTENTIAL.
                                                                                                                                                                                                                                                                               homologue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 242.5; DB 1; Length 269; 31.0%; Pred. No. 8.1e-08;
                                                                                                                                                                                                                                                                                                          Immunology 90:294-300(1997).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29983 MW; 746903F30F95F387 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 X TNFR-CYS.
                269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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TNFR-CYS 4
N-LINKED (
N-LINKED (
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U57745; AAC48710.1; -. HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%;
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                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
                                                                                                                                                                     Bovidae; Bovinae; Bos.
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103
144
187
153
180
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104
145
153
180
269 AA;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P25942
                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
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SEQUENCE
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CD40_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96437016; PubMed-8839832;
Horie R., Ito K., Tatewaki M., Nagai M., Aizawa S.,
Higashihara M., Ishida T., Inoue J., Takizawa H., Watanabe T.;
Higashihara M., Ishida T., Inoue J., Takizawa H., Watanabe T.;
A variant CD30 protein lacking extracellular and transmembrane domain is induced in HL-60 by tetradecancylphorbol acetate and is expressed in alveolar macrophages.";
Blood 88:2422-2432(1996).
I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
--- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
--- ROLE IN THE REGULATION OF CELLULAR GROWTH AND TRANSFORMATION OF
                                                                                                                                                                                                                                                                                                                                                         TISSUE-Lymphoid;
MEDLINE-92154659; PubMed-1310894;
MEDLINE-92154659; PubMed-1310894;
Duerkop H., Latza U., Hummel M., Eitelbach F., Seed B., Stein H.;
"Molecular cloning and expression of a new member of the nerve growth factor receptor family that is characteristic for Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Opposite effects of the CD30 ligand are not due to CD30 mutations: results from cDNA cloning and sequence comparison of the CD30 antigen from different sources.";
                                                                                                            01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN CD30) (KI-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- ALTERNATIVE PRODUCTS: A SHORTER CYTOFLASMIC FORM C30V WHICH IS
- OLLY EXPRESSED IN ALVEOLAR MACROPHAGES IS PRODUCED BY THE USE
OF AN ALTERNATIVE INITIATION CODON IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: PHOSPHORYLATED ON SERINE AND TYROSINE RESIDUES.
-!- DISEASE: WOST SPECIFIC HODGKIN'S DISEASE ASSOCIATED ANTIGEN.
-!- SIMILARITY: CONTAINS A LA-NGFKTNER-TYPE CYSTEINE-RICH REGION.
-!- DATABASE: NAME-PROW, NOTE-CD guide CD30 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd30.htm".
                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95089787; PubMed-7527901;
Jung W., Krueger S., Renner C., Gause A., Sahin U., Trumper L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVATED LYMPHOBLASTS. REGULATES GENE EXPRESSION THROUGH ACTIVATION OF NFKB.
                                           595 AA.
                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A. (VARIANT C30V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Immunol. 31:1329-1334(1994).
                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M83554; AAA51947.1; -. EMBL; S75768; AAD14188.1; -. EMBL; D86042; BAA12973.1; -.
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 68:421-427(1992).
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                 INFRSF8 OR CD30.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                         CD30_HUMAN
P28908;
                                                                                                                                                                            ANTIGEN)
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RESULT 13
CD30_HUMAN
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Query Match
Best Local S:
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                     SAVNSCARCFFHSVCPAGMIVKFPGTAQKNTVCEPASPGVSPACASPENCKEPSSGTIPQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----STDICRPHQICNVVAIPG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 SPTQSLLVDSQASKTLPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVVGSSAFLLCH 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 KTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCAL 128
                                                                                                                                                                                                                                                                                  ; Score 241; DB 1; Length 595;
; Pred. No. 2.1e-07;
41; Mismatches 183; Indels 176; Gaps
                                                                                                                                                                                                                                                                                                                                     7 ALGLLFLGALRAFPQDRPFE-----DTCHGNPSHYXDKAVRRCCYRCPMGLFPTQQCP 59
                                                                                                                                                                                                                                                                                                                         11 AVGLELWAAAHALPAQVAFTPYAPEPGSTC--RLREYYDQTAQMCCSKCSPGQHAKVFCT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 APSTSFL------LPMGPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 VKKKPLCLQREAKVPHL--PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 AKPTPVSPATSSASTMPVRGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQPCPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 NASMDAVCTSTSPTRSMAPGAVHLPQ-----PVSTRSQHTQPTPE----PST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CARCVPYPICAAETVTKPQDMAEKDTTFEAPPLGTOPD-CNPTPENGEAPAST
                                                                                                                                                                                                                         PRO/SER/THR-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
             InterPro; IPR001368; TNFR_c6.
InterPro; IPR001268; TNFR_c6.
SMART; SM00208; TNFR, 4.
PROSITE; PS00052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat; Phosphorylation; Alternative initiation.
SIGNAL 1
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                                                                                                         CD30L RECEPTOR, VARIANT C30V FOR VARIANT C30V.
                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                      7A407CC78A6E0BC8 CRC64
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                                                                                               CD30L RECEPTOR.
                                                                                                                                                      6 X TWER-CYS.
TWER-CYS 1.
TWER-CYS 2.
TWER-CYS 3.
TWER-CYS 5.
TWER-CYS 5.
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                                                                                                                                     POTENTIAL.
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Best Local Similarity 22.0%;
Matches 113; Conservative 4
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276
595 AA;
HSSP; P19438; 1NCF.
MIM; 153243; -.
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271 AA

PRT;

STANDARD;

OX40_RAT

RESULT 14 OX40_RAT ID OX40_R

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                       Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PGQHAKVFCTKTSDTVCDSCEDSTYTQLWNW--VPECLSCGSRCSSDQVETQACTREQNR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VW----AALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYD--QTAQMCCSKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSEL--KQNCTPTEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETS - - - DVVCKPCAPGTFSNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. ..) (POTENTIAL). C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00208; TNFR; 3.
PROSTIE; PS0065; TNFR_NGFR_1; 3.
PROSTIE; PS50060; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.3%; Score 229.5; DB 1; Length 271; 27.1%; Pred. No. 4.6e-07; tive 28; Mismatches 88; Indels 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (F
01-APR-1990 (Rel. 14, Created)
1-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
0x40L RECEPTOR PRECURSOR (0X40 ANTIGEN) (MRC 0X40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OX40L RECEPTOR.
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TNFR-CYS 1.
                                                                                                                                                                                                                       TISSUE-T-cell;
MEDLINE-90214614; PubMed-2157591;
Arclay A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17037; CAA34897.1; -. PIR; S08036; S08036. PIR; S12783; S12783. IN-ESP; P25942; ICDF. Interpro; IPR001368; TNFR_66; Pfam; PF00020; TNFR_66; 3. Probom; PD000771; TNFR_66; 1.
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                                                                               TNFRSF4 OR TXGP1L OR OX40. Rattus norvegicus (Rat).
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103
1143
271 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID-10116;
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174 SSTDICRPHQICNV----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT-- 227
               Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J., Claassen E., Noelle R.J., Fell H.; "Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene structure and chromosomal localization of the mouse homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of rat OX40 protein.";

Eur. J. Immunol. 25:926-930(1995).

- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUMILARITY: CONTAINS A LA-NGFR/TWFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                          228 QPTPEPSTA-----PSTSFLL-PMGPSPPAEGSTGDFALPVGLIVGVTA 270
                                                                             MEDLINE-95255413; PubMed-7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL) POTENTIAL.
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
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                                                                                                                                                              OX40_MOUSE STANDARD; PRT; 272 AA. P47741; 01-FEB-1996 (Rel. 33, Last sequence update) 01-FEB-1996 (Rel. 40, Last annotation update) OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN). THERSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OX40L RECEPTOR.
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InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 1.
Probom; PD000771; TNFR_c6; 1.
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272
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C
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                                                                                                                                                                                                                                                                                                                                                                                61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNW--VPECLSCGSRCSSDQVETQACTREQNRIC 118
                                                                                                                                                                                                                                                                                                                                                                                                                              231 PEPSTA-----PSTSFLLPMGPSPPA----EGSTGDFALPVGLIVGVTA-LGLLIIGVV 279
                                                                                                                     Gaps
                                                                                                                                                      6 VW----AALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                                                                                      3 WWVQQPTALLLLALTLGVTARRL------NCVKHTY--PSGHKCCRECQPG 45
                                                                                                                                                                                                                                                                                        119 TCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETS---DVVCKPCAPGTFSNTTSS
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                  s; Score 223.5; DB 1; Length 272;
s; Pred. No. 1e-06;
32; Mismatches 97; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 12, 2002, 12:51:31 Job time: 207 sec
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144 N-
15 A
30153 MW;
                                                                                                                   88; Conservative
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272 AA;
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CARBOHYD
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Run on:

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057115 cowpox viru
057097 camelpox vi
057112 variola vir
065407 variola vir
057118 cowpox viru
057118 cowpox viru
057110 cowpox viru
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057300 cetromelia
057092 cetromelia
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MEDLINE-91370690; PubMed-1966549;
A Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
A Brockhaus M., Lesslauer W.;
A Brockhaus M., Lesslauer W.;
Two human TW receptors have similar extracellular, but distinct
intracellular, domain sequences.";
Cytokine 2:231-237(1990).

REMBL: S63368; AAB19824.2; -.
RISP: P25942; IACP.
RITHE-PC: IPRO01368; TWFR_C6.
Pfam: PF00020; TWFR_C6; 4.
RISP: PCDOmi PD000771; TWFR_C6; 1.
RMART: SM000208; TWFR_C6; 1.
RMART: SM000208; TWFR_C6; 1.
RMART: SM000208; TWFR_C6; 1.
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
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ive 0; Mismatches 0;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                       EQNRICTCRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSN
                                                                                       TTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTP
                                                                                                                                                EPSTAPSTSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKK
                                                                                                                                                                                                         291 PLCLQREAKVPHLPADKARGTQGPEQQHLLITAP·SSSSSSLESSASALDRRAPTRNQPQ
                                                                                                                                                                                                                                                                     350 APGV-EASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDT
                                                                                                                                                                                                                                                                                     ARVMAEAQGSQEARASSRISDSSHGSHGTHVVVTCIVNVCSSSDHSSQCSSQASATVGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSPGQHAKVFCTKTSDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powell B.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                                                                                                                                                                                                                                                                                                              461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 459;
                                                                                                                                                                                                                                                                                                                                            DSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
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F -> I.
F -> I.
S -> E.
Y -> C.
W; 6C5ID2CF1C4626DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q62327;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.8%; Score 1477; DB 11; 63.8%; Pred. No. 3.2e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                  459
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NOD;
MEDLINE=95178848; PubMed=7873884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD000771; TWFR_C6; 1.
SMART; SM0208; TNFR; 4.
PROSITE; PS00552; TWFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
NON TER 1
VARIANT 87 87 S
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ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamm. Genome 5:726-727(1994).
EMBL: X76401; CAA53981.1; -.
HSSP: P19438; INCF.
InterPro; IPR001368; TWFR_G6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.8<sup>3</sup>
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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268
345
421
459
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VARIANT
SEQUENCE
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                                                                                                                                                                                                                                                                                                 GQHAKVFCTKTSDTVC-DS-----CEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTR 112
                                                                                                     PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%; Score 1498; DB 11; Length 482;
62.8%; Pred. No. 8e-108;
.ive 49; Mismatches 111; Indels 16; Gaps
GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSAS
                                                                                                                                                                                                                          ALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQ
                                                                                                                                                                                                                                        CSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDA
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                                           SDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure
Characterization of the two Transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00020; TNFR_c6; 4.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM0208; TNFR; 4.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_1; 2.

SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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EMBL; Y14619; CAA74969.1; -

EMBL; Y14621; CAA74969.1; JOINED.

EMBL; Y14622; CAA74969.1; JOINED.

EMBL; Y14622; CAA74969.1; JOINED.

EMBL; Y14629; CAA74969.1; JOINED.

EMBL; Y14679; CAA74969.1; JOINED.

HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001368; TNFR_c6.
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17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P80 TNF-ALPHA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                      425
                                                                                                                                                                                                                                                                                                                                           GMKPS 461
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                             GMKPS
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Best Local 3
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Matches
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147 FGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PSAGPRIIYVSQPEPTRSQPMGQEPGPSQTPHIP--VSLGSTPIIEPSITGGISLPIGLI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 429
                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 | SPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 VGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLIT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komata T., Tsuchiya N., Matsushita M., Tokunaga K.; "New poliymorphism within the extracellular region of TNFR2. Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB030952; BAA89055.1; -.
                                                                                                                                                                                                                                                                               Balchak S.K., Marcinkiewicz J.L.;
Evidence for the Presence of Tunor Necrosis Factor Alpha
During Ovarian Development in the Rat.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF142499; AAD30148.1; -...
InterPro: IPR001368; TNFR.c6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.5e-30;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
175 175
175 AA; 18201 MW; 499EEADAAB21ED8B CRC64;
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92 AA; 9530 MW; 89BEDE40B7CC4FE1 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAMBRIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%; Score 482; DB 4;
100.0%; Pred. No. 3.5e-30
:1ve 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%; Score 503.5; DB 1
55.9%; Pred. No. 1.4e-31;
iive 23; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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                                                                                                                                                                                                                                                           STRAIN-SPRAGUE DAWLEY; TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10116;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
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SEQUENCE
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Best Local S
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                                                                                   CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 PGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFR 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                 ASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                               ST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQ
                                                                                                                                                                                                                                                                                                                                                                                                                          GPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EASGAGEARASTGSSDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ118D24.3 (TUMOR NECROSIS FACTOR RECEPTOR 2 (75 KDA) (TNF-PROTEIN 2, TBPII, TNF-R2, CD120B, TNFBR)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16449 MW; E6C96E774B5CF7B0 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%; Score 826; DB 4; I
llarity 100.0%; Pred. No. 1.8e-56;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPYETTETL -- QSHEKPLPLCVPDMGMKPS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL031276; CAA20343.1;
NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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Matches 161;
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SEQUENCE
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91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                         81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140
                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                  PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV
                                                                                                 24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL
                                                                                                                                                                                                            151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN-----VVAIPGNASMDAVCTS
              1.4e-22;
ches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U88144; AAB94359.1; -.
EMBL; U87994; AAB94355.1; -.
EMBL; U87995; AAB94356.1; -.
EMBL; U87995; AAB94365.1; -.
EMBL; U87995; AAB94366.1; -.
EMBL; U88143; AAB94368.1; -.
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2.
CBD2C949ED2B8E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                         349 AA
            Pred. No. 1.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
41.8%; Pic. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 349 AA; 38295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001368; TNFR_c6. Pfam; PF00020; TNFR_c6; 2. ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Conservative
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkeypox virus.
                                                                                                                                                                                                                                                                                203 TSPT 206
                                                                                                                                                                                                                                                                                                           197 TTTT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTT 200
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                                                                                                                                                                                                                                                                                                                                                                                                         057291
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              Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPKPSTAPSTSFLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                Komata T., Tsuchiya N., Matsushita M., Tokunaga K.;
"New poliymorphism within the extracellular region of TNFR2.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030951; BAA89054.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 409; DB 4; Lengtn , ...
Pred. No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ZAIRE-1977 (77-0666);
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U87845; AAB94362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSF; k.23-42, L.2...
InterPro: IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR_c6; 1.
SMART; SM00208; TNFR, 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEOUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3A219A37EAFE0719 CRC64;
                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 390.5; DB 12;
                                                                                                                       78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
           61 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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48
78
                                                                                                                                                                                                                                             Homo sapiens (Human).
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
78
78 AA;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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RESULT 057101

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NON_TER SEQUENCE

Receptor

NON_TER VARIANT

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N
                                                                                                                                                                                                                                                    91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                               151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN------VVAIPGNASMDAVCTS 202
                                                             Gaps
                                                                                                                                           24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80
                                                                                                            31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                          15;
Ouery Match 15.8%; Score 389.5; DB 12; Length 349; Best Local Similarity 41.8%; Pred. No. 1.7e-22;
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Query Match

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9

80

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81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                         31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                 24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRP--HQICNVVAI-----PGNASMDAVCTST
                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                               Length 348;
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                                                                                                                                                                                                                                                                                                                          Indels
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Submitted (JAN-11997) to the EMBL/GenBank/DDBJ databases
EMBL, 197847, AAB94364.1; -
HSSP; P25942; 1CDF.
                                                                                                                                                               54019521556C2D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34A5E668B27907B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                     15.8%; Score 389; DB 12; 42.1%; Pred. No. 1.8e-22; tive 22; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.8%; Score 389; DB 12; Best Local Similarity 42.1%; Pred. No. 1.8e-22; Matches 77; Conservative 22; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence 01-JUN-2001 (TrEMBLrel. 17, Last annotatic TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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Pfam; PF00020; TWFR_c6; 2.
ProDom; PD000771; TWFR_c6; 1.
PMART; SM0208; TWFR; 2.
PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 2.
SEQUENCE 348 AA; 38184 MW; 34A5
Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR, 2.
PROSITE; PS00652; TNFR_NGFR_1; 2
PROSITE; PS0050; TNFR_NGFR_2; SEQUENCE 348 AA; 38212 MW; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ZAIRE-1979 (79-0005);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O57103;
01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                        Query Match 15.8
Best Local Similarity 42.1
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monkeypox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |
197 TTT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN------VVAIPGNASMDAVCTS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkeypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loparev V.N., Parsons J.M., Esposito J.J.;
Lucare Lucare AAB9363.1;
REMBL, 1087846; AAB9363.1;
REMBL, 1087846; AAB9363.1;
REMBL, 1087846; AAB9368; TWR_C6.
REMBL, 1087846; AAB, 188308 MW; CBDZC949F994C59C CRC64;
REMOSITE; PS50065; TWRR_NGFR_1; 2.
REQUENCE 349 AA; 38308 MW; CBDZC949F994C59C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
LOPATEV V.N., PALSONS J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U88543; AAB94378.1; -.
EMBL; U87841; AAB94358.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.
2.
CBD2C949F994C59C CRC64;
                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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                                                                                                   349 AA
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                                                                                                   PRT;
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STRAIN-BENIN-1978 (78-3945);
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                                                                                                   PRELIMINARY;
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NCBI_TaxID=10244;
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         RESULT 10 4
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10 57277
AC 057277
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DT 01-JUN
DT 01-J
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to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1997) to t}
EMBL; U87843; AAB94360.1;
HSSP; P25942; 1CDF.
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Best Local Similarity 39.7%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                        Best Local Similarity 41.8
Matches 77; Conservative
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Orthopoxvirus
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057284
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRP--HQICNVVAI-----PGNASMDAVCTST 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ZAIRE-1970 (CONGO-8);
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (FBB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 1088142; AAB94367.1;
HSSP: P25942; ICDF.
InterPro: IPR011368; TNFR_C6.
Pfam: PF000207 TNFR_C6; 2.
ProDom: PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.
2.
E555979057DEC91F CRC64;
                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                             348 AA.
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STRAIN=SIERRA LEONE-1970 (70-0266);
Loparev V.N., Parsons J.M., Esposito J.J.;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotatio
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 348 AA; 38212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                             PRELIMINARY;
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nes 77; Conserva
                                                                                                                                                                                                                                                                                                                                                                               Orthopoxvirus.
NCBI_TaxID=10244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB TaxID=10244;
                                                                                                                                                                                                                                                                                                                                   Monkeypox virus.
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TTT 199
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TTT 199
                      SPT 206
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Matches
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91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
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                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                           24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL
                                                                                                                                                                                                                                                                                                                                                             31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV
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                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                Length 349;
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                                                                                                                                                                                                                                             15.7%; Score 386.5; DB 12; Length
41.8%; Pred. No. 2.8e-22;
tive 21; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRALH-1992 (CP-5), SOMALIA-1978;
LOPARN-V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                          2.
2.
FE449028CC933F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.
2.
EA412AEE86E090E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       057284;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%; Score 385; DB 12; 39.7%; Pred. No. 3.7e-22; iive 19; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
InterPro; IPR001368; TWFR_c6.
Promom; P00020; TWFR_c6; 2.
Probom; P000071; TWFR_c6; 1.
SMART; SM00208; TWFR; 2.
PROSITE; P500552; TWFR_NGFR_1; 2.
PROSITE; P550050; TWFR_NGFR_1; 2.
SEQUENCE 349 AA; 38321 MW; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; PR001368; TWFR_c6.
Pfam; PF00020; TWFR_c6; 2.
ProDom; PD000771; TWFR_c6; 1.
SMART; SM00208; TWFR, 2.
PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_1; 2.
SEQUENCE 349 AA; 38036 MW; EF
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EMBL; U87837; AAB94354.1; -.
HSSP; P25942; ICDF.
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80 pPACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCILKGSSGCKACVSQTKCGIGYGV 139.
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191 TSCTRTTTT 199
                                               198 AVCTSTSPT 206
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Search completed: February 12, 2002, 12:50:47 Job time: 214 sec

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Tumour necrosis factor receptor; immune response; inflammation; cachexia; septic shock.
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/label- TNF receptor
258..287
/label- transmembrane region
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                                                           AAB50080
AAR51003
AAR24016
AAY94718
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AAW89234
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AAB50084
AAY77462
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AAR11142
AAB70001
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AAR77421
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AAB37684
AAR70111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TNF-R deduced from clone 1.
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89US-0405370.
89US-0421417.
 (first entry)
 (IMMU-) IMMUNEX CORP
                              10-MAY-1990;
11-SEP-1989;
13-OCT-1989;
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AAR11141
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 (without alignments)
1375.817 Million cell updates/sec
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Fibroblast derived
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Death receptor. H
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p75 Tumour Necrosi
Sequence of human
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                                                                                                                                                                                             2400
1 MAPVAVWAALAVGLELWAAA......GSTEEKPLPLGVPDAGMKPS 461
                                                                                                         February 12, 2002, 12:44:58; Search time 24.82 Seconds
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| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseqy/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseqy/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseqy/geneseqp/AA1985.DAT:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               522463 segs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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AAR72504
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10 9 10 110

Score

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Result

Peptide fragment of Tumour necrosis fa Human 40 kba TNF 1 Rat TNFR (p80) ext TNFR FC fusion pro Rodent protein seq Truncated soluble Human TNF-II pepti Human 40 kba TNF 1

TNF-R extracellula Human TNF-R extrac Human tumour necro TBPII-GBP 130 fust TNF-R-GBP 130 fust

Wild type N-termna Amino acid sequenc Amino acid sequenc Human soluble tumo Tumour necrosis fa Tumour necrosis in A K108R/K120R muta

TNF-R deduced from STNFR(075):Fc fus1 TNFR:Fc fus1on pro

Human tumour necro

Sequence of a reco Fusion protein TNF Human type 2 tumou

Tnfr2 protein. Un Primate protein se Human type 2 tumou BamTP delta53 nerv

Human 40 kDa TNF 1

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pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;
                   autoimmune dysfunction.
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                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
                                                                                                                                                                                                                                                                                                                                                                                                                 phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsghtgptpepstapsts 240
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                                                                                                                                                                                                                                                                                                                QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
                                                                                                                                                                                                                                                                        MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                    The sequence was deduced from a DNA sequence obtd. from a clone isolated from a library prepd. from a human fibroblast cell line, WN-26 WA4 (ATCC CCL 95.1). The clone is deposited as Accession No. 68088 under the name pCW/NOY-TNF-R. The DNA can be truncatd to produce sequences which express soluble receptor comprising residues 1-25, 1-185 or 1-163 of the protein.
                                                                                                                                                                                                                                                                                                                                                                                              PHQICONVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAFSTS
                                                                                                                                                                                                                                                                                  PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ
                                                                   encoding these used to regulate immune responses in treatment of cachexia, septic shock or side-effects of cytokine therapy.
                                                          New tumour necrosis factor -alpha and -beta receptors - and DNA
                                                                                                                                                                                                                                 DB 12; Length 461;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2468; DB 12;
100.0%; Pred. No. 1e-152;
ive 0; Mismatches 0;
          Beckmann PM;
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                                                                                                 Disclosure, Fig 2; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrablast derived TNF-R.
          Goodwin RG,
                             WPI; 1991-082230/12.
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                     AA;
                                                                                                                                                                                also AAR11142
                                        N-PSDB; AAQ10990
                                                                                                                                                                                                    461
                                                                                                                                                                                                                                                     461;
         Smith CA,
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Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, oscrebral malaria, allograft and xenograft rejection in graft verses notoimmune dysfunctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in AAR42060-61 represent human interleukin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
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Pred. No. 1e-152;
                                                                                                                                                                                            "Preferred soluble TNF-R"
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IL-1R-linker-TWF-R-linker-TWF-R or
TWF-R-linker-TWF-R
                                                                                           'note= "Signal peptide"
                                                                                                                    23..461
/note= "Mature hTNF-R"
                                             Location/Qualifiers
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Best Local Similarity
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Homo sapiens
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inflammatory diseases and autoimmune diseases
                         Claim 16; Page 24-25; 228pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel tumour necrosis factor family receptor for diagnosing and treating acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
                                                                                          FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
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                                                                                                                                RPGWYCALSKOEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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                                       PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS
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99US-0136248
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461; Conservative
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26-MAY-1999;
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The present sequence encodes human tumour necrosis factor family receptor (TNP-RII) polypeptide. The specification describes a TNF receptor designated TRI. An agonist to the TRI receptor is useful for inhibiting tumour growth, to stimulate human callular proliferation, to regulate immune response and antiviral response, to protect against the effects of ionising radiations, to protect against chlamydia infections, to regulate growth, and to treat immunodeficiencies such as in human immunodeficiency virus (HIV). An antagonist to the TRI receptor is useful for treating T-cell mediated autoimmune diseases, acquired immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft rejection, cytotoxicity, cachexia, apopticsis, and inflammation. TRI polynucleotides and polypeptides, and TRI agonists and antagonists are useful for treating cancers, cardiovascular diseases, inflammatory diseases, atherosclerosis, diabetes mellitus, neurological disorders, autoimmune diseases, for promoting angligenesis, for treating allergy, for wound healing, for regulating bone formation and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence comprises the entire 40 kD TNF inhibitor. The clone from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases.
                                                                                                                                                                                                                                                                                                                                    MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG
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                                                                                                                                                         Tumour necrosis factor inhibitor - for suppression of TNF-alpha
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                                                                                                                                                                                                                                                                                                Score 2462; DB 12;
Pred. No. 2.6e-152;
0; Mismatches 1;
                                                                                                                                                                 -beta, useful as therapeutic agent.
                                                                                                                                                                                   Disclosure; Fig 39; 142pp; English
                                                                                                                                                                                                                                                       See also AAR10986 and AAR10984
                                                                           90US-0479661.
89US-0381080.
89US-0450329.
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                                                           90AU-0058976
                                                                                                                                                                                                                                                                                                                  460; Conservative
                                                                                                               SYNE-) SYNERGEN INC
                                                                                                                              WPI; 1991-073847/11.
N-PSDB; AAQ10907.
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11-DEC-1989;
                                                          16-JUL-1990;
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The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or tetracycline-like compounds for treating and/or preventing acute inflammatory responses and diseases. Such diseases include acute inflammatory conditions associated with viral hemorrhagic diseases (including diseases caused by Bunyaviridea, Filoviridea, Flaviviridea or Arenaviridae viruses), parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune disorders, acute cardiovascular events, chronic myelogenous leukaemia and transplanted bone marrow-induced graft-versus-host disease, septic shock, immune complex-induced colitis, cerebrospinal fluid inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis, inflammatory responses associated with trauma, systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
                                                                                                                                                                                                                                              Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor; p75 receptor; antinflammatory; haemostatic; antibacterial; sepsis; immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia; neuroprotective; respiratory; inflammation; infection; Crohn's disease; multiple sclerosis; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia; inflammatory bowel disease.
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Pred. No. 2.6e-152;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compositions comprising tetracycline or compounds for the treatment and/or prevention responses and diseases, e.g. septic shock and
                                                                                                                                                                                       p75 receptor.
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      AA.
AAB37801 standard; Protein; 461
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                                                                                                                                                                                       Human tumour necrosis factor
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99.8%;
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                                                                                                                          (first entry)
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Best Local Simi
Matches 460;
                                                                                                                          23-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pure or recombinant polypeptide which binds to a polyclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific for the mature UL14 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
                                                                                             ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
                                                                                 PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE
FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
                                                                                                                                                                                                                                                                                                                                                              UL144; death receptor; apoptosis; programmed cell death; FAS;
TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
                                                                                                                                                                               461
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                                                                                                                                                                                                                                                                                                                                        Death receptor
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Length 461;

Score 2462; DB 21; Pred. No. 2.6e-152;

99.8%; 99.8%;

Best Local Similarity

Query Match

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Nucleic acids encoding 2 human tumor necrosis factor receptor polypeptides ((FRI3) and (FRI4)), useful for the prevention, diagnosis and treatment of, e.g. cancers, acquired immune deficiency syndrome and hypohidrotic ectodermal dysphasia
                                              61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
                                                                                             121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG
             181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS
                                                                                                                                                           PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour necrosis factor receptor; TR13; TR14; infection; cancer; autoimmune disease; allergy; inflammatory disease; graft rejection; apoptosis; cardiovascular disease; aneurysm.
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99US-0149450.
99US-0149712.
99US-0153089.
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20-AUG-1999;
10-SEP-1999;
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Query Match
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                 The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TR13 and TR14. These sequences are useful in the diagnosis and treatment of many diseases, including cancer, autoimmune diseases, cardiovascular disorders, allergies, neurodegenerative diseases, graft rejection, inflammation, aneurysms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; apoptotic restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.
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                                                                                                                                                                          Human tumour necrosis factor receptor TNFR2 protein SEQ ID NO:3.
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Pred. No. 2.6e-152;
O; Mismatches 1;
Disclosure; Page 377-378; 418pp; English.
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                                                                                                                       99.8%;
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                                                                                                                                           460; Conservative
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The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antilnilammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain heematopoletic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID colynucleotides, proteins, antibodies, agonists and antagonists are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID colynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased cells of the propertion of the proper
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding a TRID polypeptide, also referred to as t
necrosis factor receptor 5, useful in the diagnosis, treatment
prevention of cancer, autoimmune disorders and viral infection
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                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
18-MAY-2000; 2000WO-US13515.
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                                                                                                                                                                                        A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane aused in the production of a pharmaceutical composition for increasing the inhibitory effect of a
                                           361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ
                                                                                                            FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
                                                                                                                                                                        301 PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE
- used to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
                                                                                                                                                                                                                                                                                                                 421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Unidentified amino acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor (TNF) receptor ligand inhibitory effect of a soluble TNF receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p75 Tumour Necrosis Factor Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the precursor for 40 kbg TNF inhibitor. The 40 kbg TNF inhibitor can inhibit both TNF alpha and beta (lymphotoxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by
361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssgasstmgdtdsspsespkdeg 420
                                                                                                                                                                                                                                                               TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; IL-1; inflammatory disease; degenerative disease; human; lymphotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
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                           Score 2462; DB 22;
Pred. No. 2.6e-152;
0; Mismatches 1;
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RW, Vannice J, Kohno T;
                                                                                                                                                                                                                                  Human 40 kDa TNF inhibitor precursor.
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99.8%;
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89US-0450329.
90US-0479661.
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Vanderslice RW,
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                                                                                                                            RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
                                                                                                                                                        PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
                                                                                                                                                                                   FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
                                                                                                                                                                                                              PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
                                                                                                                                                                                                                                         ARASTGSSDSSPGGHGTQ-----VNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPS 413
                                                         Gaps
                                                                           MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                                                                                          therapy
 This sequence
                                                         14;
                                         Length 461;
                                                                                                                                                                                                                                                                                                                                                                                 type I; TNFRI; arthritis
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence of human tumour necrosis factor receptor type (TNPRI).
                                                                                                                                                                                                                                                                           ESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
 family.
                                          Score 2394; DB 16;
Pred. No. 6.7e-148;
                                                        0; Mismatches
soluble receptor of the TNF/NGF receptor is the sequence of the p75 TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                    AAR51002 standard; Protein; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                        mature
                                                                                                                                                                                                                                                                                                                                                                                                                    l..22
/label= signal
                                          97.0%;
96.4%;
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 22..461
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                 Similarity
                      AA;
                     461
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1992;
                                                                                                                                                                                                                                                                                                                                               07-0CT-1994
                                                       451;
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                                         Query Match
Best Local S:
Matches 451;
                     Sequence
                                                                                                                                                                                                                                                                                                                                  AAR51002;
                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast cell line WI-26 VA4. The mature full-length TWRI is a glycoprotein having a mol. Wt. of about 75-80 kba.The cloning of the cDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1 is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The preferred TNFRs of the present invention are soluble forms of TNFRI and TNFRI having at least 20 AAS. Soluble TNFR constructs are devoid of a transmembrane region but retain the ability to bind TNF. Examples of soluble TNFRs are huTNFRIdelta185 and huTNFRIGHLA183 which encode respectively AAS 1-235,1-185 and 1-163 of AAR51002. An equivalent soluble TNFR is huTNFRIGHLA18 wherein x is selected from any one of AAS 163-235 of AAR51002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ
                                                                                                                            TNF mediated inflammatory diseases with TNF antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                      esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2376; DB 15;
Pred. No. 9.9e-147;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
                                                                                                                                                                                                                            Disclosure; Page 28-30; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
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96.78;
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Smith CA;
                                              WPI; 1994-118172/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA;
                                                                           N-PSDB; AAQ45224
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71 SDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
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241 tqgpeqqhllitapssssssssasaldrraptrnqpqapgveasgagearastgssad 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partial amino acid sequences were determined for the 55 and 75kD TNF-BPS (see AARIJO72-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda 9t11. Postitive clones were identified and sequenced. Repeated sequencing showed a discrepancy at position 7 such that the third codon encodes either Thr or Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lesslauer W, Lotscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour Necrosis Factor; binding proteins; septic she autoimmune glomerulonephritis; lymphokine; cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.1%; Score 2050.5; DB 1
98.7%; Pred. No. 1.1e-125;
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                                                                                                                                                               461
                                                                                                                                                                                           100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 
                                                                                                                                                               430 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ser, Thr
                                                                                                                                                                                                                                                                                                                                                        AAR11605 standard; Protein; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 75kD TNF-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dembic Z, Gentz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90CH-0001347.
89CH-0003319.
90CH-0000746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel homogeneous insoluble proteins (I), their (in)soluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNR). The products of the invention have anti-filammatory and antimalarial activity. (I) and (Ia) are used (i) to treat diseases in which TNR is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (ii) to purify TNR; (iii) to identify TNR (ant)agonists and (iv) for diagnostic determination of TNR in body fluids. Antibodies raised against (I) are used for affinity purification of (I). This sequence represents a tumour necrosis factor binding protein fragment described in the method
                                               Tumour necrosis factor binding protein; TNF; insoluble protein; agonist; anti-inflammatory; antimalarial; treatment; septic shock; inflammation; autoimmune glomerulonephritis; cerebral malaria; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDIVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP
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                                                                                                                                                                                                                                                                                                /note= "Partial sequence, no start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New insoluble proteins, and fragments, that bind to tumor ne factor, used to treat e.g. septic shock or cerebral malaria
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Human tumour necrosis factor binding protein fragment.
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98.7%;
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89CH-0003319.
90CH-0000746.
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                                                                                                                                                                                         Homo sapiens
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Schlaeger
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AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARG 310
                                                                                                                                                                                                 TQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSS-D 369
                                                                                                                                                                                                                  tggpegghllitapsssssslessasaldrraptrngpgapgveasgagearastgssad 300
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rom a murine T helper cell line, 789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumour necrosis factor -alpha and -beta receptors - and DNA encoding these used to regulate immune responses in treatment of cachexia, septic shock or side-effects of cytokine therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor receptor; immune response; inflammation;
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/label= signal sequence
234..265
/label= transmembrane region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11142 standard; Protein; 474
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89US-0405370.
89US-0421417.
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N-PSDB; AAQ10991.
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11-SEP-1989;
13-OCT-1989;
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New recombinant viral vectors comprising a single-stranded heterologous nucleotide sequence have a region that forms intrastrand base pairing, useful in gene therapy and genomics screening -
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                                                                                                                                                                                         239
                                                                                                                                                                  60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
                                                                                                                                                                                                                                                  CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
                                                                                                                                                                                                                                                                                                                                  CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
                                                                                                                                                                                                                                                                                                                                                                                                                239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
                                            Gaps
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                                                                                    MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP
                                                                                                         AKVPHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGV-EAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP
                                            8
      474;
    Length
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
  Score 1506; DB 12;
Pred. No. 3.3e-90;
0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                          50;
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61.0%;
62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sTNFR(075):Fc fusion protein.
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                                              Conservative
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                         Similarity
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                                              292;
    Query Match
Best Local S:
Matches 292,
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The present sequence is a fusion protein of tumour necrosis factor receptor (TNRN) and the constant region of an immunoglobulin molecule (FC), denoted SINR(075):Fc. A recombinant adeno-associated virus (rAAV) vector encoding the present sequence was used to infect a rat model of arthritis. The rats showed a significant reduction in arthritis symptoms compared with control groups. This was performed as an example. Illustrating an invention providing a new recombinant viral vector. The vector comprises a single-stranded heterologous nucleotide sequence having a region that forms intrastrand base pairs so that the expression of a coding region of the heterologous sequence is enhanced. The recombinant viral vector is useful in gene therapy and genomics screening. The vectors may also be used in the transfection, transduction and expression of a sequence of interest in a host cell and in the the accumulation of the gene product of interest is reduced to days rather than weeks since the vectors can efficiently and rapidly form complex templates for transcription.
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64.5%; Pred. No. 2e-85;
iive 22; Mismatches 67;
Example 13; Fig 10; 72pp; English.
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Best Local Similarity 64.5'
Matches 289; Conservative
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Search completed: February 12, 2002, 12:47:38 Job time: 160 sec

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APPLICANT: Jacobs, Cindy A.:
APPLICANT: Jacobs, Cindy A.:
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TWF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 2468; DB 1; Best Local Similarity 100.0%; Pred. No. 4.2e-173; Matches 461; Conservative 0; Mismatches 0;
                         US-09-006-353A-11
US-09-006-353A-14
US-08-292-549-4
US-08-292-549-4
US-08-791-02207-4
US-08-791-02207-4
US-09-042-796-2
US-09-286-529-17
US-09-286-529-17
US-09-286-529-20
US-09-286-529-20
US-08-974-022-6
US-08-974-6-6
US-08-795-445A-6
US-08-795-445A-6
US-08-795-445A-6
US-08-795-445A-6
US-08-795-445A-6
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                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wight, Christopher L. RECISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAR: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08385229
; Patent No. 5605690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 461 amino acids TYPE: amino acid
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CITY: Seattle
CITY: Washington
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MOLECULE TYPE:
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Sequence 7, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 48, Appli
Sequence 5, Appli
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Sequence 13, Appli
Sequence 13, Appli
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653.687 Million cell updates/sec
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                                                                                                       February 12, 2002, 12:45:28; Search time 15.87 Seconds
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                            Compugen Ltd
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US-08-795-447A-48
US-08-795-447A-48
US-08-995-446B-48
US-08-219-237B-5
US-08-476-862-4
US-08-476-862-4
US-08-476-862-4
US-08-476-862-5
US-08-476-862-5
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US-09-006-353A-4
US-08-650-000-4
US-09-042-785A-8
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US-08-243-010-1
US-09-326-394-4
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-476-862-2
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                                                                                                                                                                                                                                                                          212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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Maximum DB
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FILING DATE: 10-MAY-1990 ATTORNEY/AGENT INFORMATION:
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QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Snith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                         VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
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FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
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51 University Street
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PRIOR APPLICATION DATA:
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PRACE APPLICATION DATA:
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STREET: 51 carray: Seattle
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Pred. No. 4.2e-173;
                                                                                                                                                                                                                                                                                                                                                              0
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NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
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APPLICANT: WALLACHH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, IGOR
APPLICANT: METT, IGOR
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
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STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                             100.0%; Scc
100.0%; Pro
                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 287-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08477347; Patent No. 6232446
                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 461; Conservative
                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: D.C.
COUNTRY: USA
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US-08-477-347-3
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APPLICANT: BIGDA, Jacek
APPLICANT: BEEFFSKY, IGOR
METT, IGOR
APPLICANT: ENGELMANN, HARTMUL
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2468; DB 4;
100.0%; Pred. No. 4.2e-173;
live 0; Mismatches 0;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                        US/08/477,347
                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/115,685
                                                                                                                                                                                                            APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY-AGENT INFORMATION:
NAME: TOWNSEND, G. KEVIN
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-476-862-2; Sequence 2, Application US/08476862; Sequence 2, Application US/08476862; Patent No. 6262239; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 461 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 461; Conservative
                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-477-347-3
                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                          APPLICATION NUMBER:
                                                                                                        FILING DATE: CLASSIFICATION:
                                                                                                                                                                               FILING DATE:
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61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
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                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2468; DB 4; 100.0%; Pred. No. 4.2e-173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: WALLACH-12A TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TITLE OF INVENTION: THE INHIBITORS NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA: 1L 94039
FILING DATE: 06-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-476-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                        Washington
                                                                                                                               USA
                                                                                                                                          20004
                                                                                                            STATE: D.C
                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                          STREET:
                                                                                                                             COUNTRY:
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Query Match
Best Local Similarity
                                                                             GENERAL INFORMATION:
                                                                                                                                                                                 CITY: Boston
STATE: Massac
                                                                                                                                                                                                              USA
                                                                                                                                                                                                                          ZIP: 02109
                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                       US-09-042-785A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-042-785A-7
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                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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                                       PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE
                                                                             361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ
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                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
                                                                                                                                                                                                                        Patent No. 5395760
APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red. No. 4.2e-173;
Mismatches
                                                                                                                                              421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                 421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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Pred. No. 4.
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
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100.0%;
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Best Local Similarity
Matches 461; Conserv
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5395760-2
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61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
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                                                                                THE THE RECEPTOR SUPERFAMILY
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Pred. No. 1.2e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                          APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400.
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
                                                                                                                                                               LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD, STREET: 28 State Street
; Sequence 7, Application US/09042785A; Patent No. 6194151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 461 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                      NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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301 PHLPADKARGTQGPEQQHLLITAPSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
                                                                                                                                                                                                                                              361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
                                                                                                                                                                                                                                                                               241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
                                                                                                                                                       APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                                                                                                                                                                                                                                                                         421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: US/08/038,765 APPLICATION NUMBER: US/08/038,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 523,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 403,241 FILING DATE: 05-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08650000 Patent No. 5945397 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOC/MC-COMPUTER: PC-DOC/MC-MC-COMPUTER: PC-DOC/MC-COMPUTER: PC-DOC/MC-DOC/MC-COMPUTER: PC-DOC/MC-COMPUTER: PC-DOC/MC-COMPUTER: PC-DOC/MC-COMPUTER: PC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/MC-DOC/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-MAY-1990 ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
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ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
                                                                                                                       421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
                                                                                                                                                       421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: HUMAN GENOME SCIENCES, INC. 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09006353A Patent No. 6261801
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 461 amino acids
TYPE: amino acid
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APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: MD
COUNTRY: US
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                                                                                 Gaps
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                                                                                                                   1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
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APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                      GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP
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                                               Length 474;
                                                                                50; Mismatches 114; Indels
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APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                               Score 1512; DB 2;
Pred. No. 3.8e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: LAHIVE & COCKFIELD, LLP 28 State Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                61.3%;
63.0%;
                                                                                 Matches 293; Conservative
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CORRESPONDENCE ADDRESS:
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CITY: Bo
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US-08-650-000-4
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418
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                                                                                                                                                                                                                                                                                                                                                                               GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
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; APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
;M. PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461
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                                                                                                                                                                                                                         61.3%; Score 1512; DB 4;
63.0%; Pred. No. 3.8e-103;
iive 50; Mismatches 114;
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Pred. No. 3.8e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATE: 35
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 405,370 FILING DATE: 11-SEP-1989 APPLICATION NUMBER: 403,241 FILING DATE: 05-SEP-1989
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63.0%;
                                           TOPOLOGY: 11:00
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80
INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 474 amin.
                                                                                                                                                                                                                           Query Match 61.3
Best Local Similarity 63.0°
Matches 293; Conservative
                                                                                                                             peptide
internal
                                                                                                                               MOLECULE TYPE:
FRAGMENT TYPE:
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5395760-4
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us-09-800-909-2.rai

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58.1%; Score 1433; DB 1
64.5%; Pred. No. 2.5e-97
live 22; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I Street, N.W. CITY: Washington
: LENGTH: 518 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

US-08-385-229-4
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                                                                                                                                                             Matches 289; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                               Similarity
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APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
                                                                                                                          61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120
                                                                                                                                                                                            121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180
                                                                                                                                                                                                                                                                240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQKKKPSCLQRD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
                                                                                                                                                                                                                                             179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
                                                                                                                                                                                                                                                                                                                                                                                AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
                                                                                                                                                                                                                                                                                                                                                                                                  GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
                                                                                                             GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
                                                                                                                                                                                                                                                                                                               239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
                                                            Gaps
                                         1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
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          50; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seatle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08385229
Patent No. 5605690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wight, Christopher L. REGISTRATION NUMBER: 31,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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STATE: Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----APGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNV--CSSSDHSSQCSSQA-S 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 FNWYVDGVEVH-----NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKDYKCKVSNKALP 400
                                                         Gaps
                                                                                                                                                                    89
                                                                                                             1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                                               90 QHAKVECTKTSDIVCDSCEDSIYIQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC
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DB 1; Length 518;
                                                      67; Indels
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Patent No. 5639597

GENERAL INFORMATION:

APPLICANT: Lauffer, Leander

APPLICANT: CattLineissel, Gerd

APPLICANT: Oquendo, Patricia

TITLE OF INVENTION: Cell-free Receptor Binding Assays,

TITLE OF INVENTION: Cell-free Receptor Binding Assays,

TITLE OF INVENTION: Cell-free Receptor Binding Assays,

TITLE OF INVENTION: Production and Use Thereof

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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PRIOR APPLICATION DATA
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US-08-974-022-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Sennello, Regina M.
APPLICANT: Sennello, Regina M.
TITLE OF INVENTION: COMBINATION THERAPY USING A THE BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING THF-MEDIATED DISEASES
NUMBER OF SEQUENCES: A
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                        Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                 56.9%; Score 1404; DB 1;
100.0%; Pred. No. 3.1e-95;
Live 0; Mismatches 0;
                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 202-408-4000
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PO COMPATIBLE
COMPUTER: IB P PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09326394 Patent No. 6306820 GENERAL INFORMATION:
                                                                                                                                                                                               TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-243-010-1
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241 FLLPMGPSPPAE 252
                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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83 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 TSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD 257
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/974,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1312; DB 4;
Pred. No. 6.8e-89;
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PELING DATE: 05-00032,000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
FILING DATE: 23-AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRIOR APPLICATION NUMBER: US 60/052,023
FILING DATE: 09-011-1997
APPLICATION NUMBER: 32,1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOYLE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UNMER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/974,022
12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 48, Application US/08974022; Patent No. 6015938; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 53.2%;
Best Local Similarity 99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                        Length 227;
                                                                                                                                                                                                                                                                                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
                                                                                                                                                                                                                                                    Score 1263; DB 3;
Pred. No. 2.5e-85;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOYLE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/08795445A Patent No. 6284485 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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APPLICATION NUMBER: 08/577,788
                                                                                  48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        51.2%;
                                             NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                      Query Match 51.2
Best Local Similarity 99.6
Matches 226; Conservative
                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-974-022-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 91320-1789
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                   FILING DATE
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                                                                                        Length 227;
                                                                                                                       Indels
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                                                                                        Score 1263; DB 4;
Pred. No. 2.5e-85;
0; Mismatches 1;
                                                                                          51.2%;
99.6%;
                                                                                                                         Conservative
             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                        Query Match
Best Local Similarity
Matches 226; Conserv
STRANDEDNESS:
STRANDEDNES

TOPOLOGY:

MOLECULE TYPE
US-08-795-445A-48
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Search completed: February 12, 2002, 12:48:00 Job time: 152 sec

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(without alignments)
136.983 Million cell updates/sec
                                                                                                                                                       February 12, 2002, 13:02:20 ; Search time 12.79 Seconds
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                             Run on:
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219241 segs, 76174552 residues US-09-800-909-2_COPY_163_185 134 1 PCAPGTFSNTTSSTDICRPHQIC 23 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

4466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ca2+/calmodulin-de	T-cell receptor be		30K allergen - rye	on-like p	gene HEXA protein	LX-1 tumor antigen	homeodomain protei	leader peptide [im	mu-conotoxin GIIIA	antigen (clone PV1	24K antigen - Myco	9	convulsant peptide	aspartylglycosamin	paralytic peptide	paralytic peptide	substance P - rain		S-locus specific g	trypsin (EC 3.4.21	virion morphogenes	S-locus specific g	self-incompatibili	mu-conotoxin GIIIB	mu-conotoxin GIIIC	exo-poly-alpha-gal	peptidylglycine mo	T-cell receptor be
SUMMARIES	ID	A42865	B49048	S47381	S38292	A60317	I54351	A39269	860565	T48881	MXKN1	JN0263	B60278	154283	A59048	137144	E39855	D39855	S23308	PQ0491	D56661	B61334	B56613	C56661	PQ0492	MXKN2	MXKN3	A48968	B38671	PH0891
	DB	7	7	7	7	7	7	~	7	7	Н	7	7	~	7	~	7	7	~	~	C	~	7	7	7	Н	Н	~	7	7
	Length	20	18	13	16	17	21	22	23	20	22	15	16	20	23	22	23	23	11	13	13	17	19	19	19	22	22	23	23	11
	Query Match	3.1	2.4	1.6	•	1.6	9.1	1.6	6.	0.1	0.1	4.	4.6	4.	7.4	•	9.0	9.0	3.7	3.7	•	٠	8.7				8.7	•	٠.	7.9
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	Score	31	30	29	29	29	29	29	28	27	27	26	26	26		വ	25.5	S	25	25	25	25	25	25	25	25	25	25	25	24
	Result No.		7	3	4	2	Q	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

T-cell receptor al hemoglobin beta-2	collagen alpha 3(I	alpha-conotoxin Pn	helothermine - Mex	paralytic peptide	paralytic peptide	tremerogen A-10 -	bma protein - Clos	R-phycoerythrin ga	36K protein 3124 -	T-cell receptor al	lutropin beta chai	vasotocin-associat	T-cell receptor al	Ig H chain V-D-J r
PH0776	C39543	B54877	A34859	F39855	G39855	JTJG0	I40663	G22565	PS0453	PH0799	B61309	A49155	PH0782	PH1634
2 0	10	7	7	7	7	-	7	7	7	7	7	~	7	7
14	21	16	70	23	23	12	12	13	13	13	14	15	15	16
17.9	. 0.	5.	5.	2.5	5.	7.2	7.2	2.7	2.7	.2	2.7	7.2	.2	7.2
17	11	13	1,	1,	7	1,	1	Ξ	17	1,	1,	17	ï	1,
24	24	23.5	23.5	23.5	23.5	23	23	23	23	23	23	23	23	23
30	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A42865 Ca2+/calmodulin-dependent myosin light chain kinase (autophosphorylation sites) - rak Ca2+/calmodulin-dependent myosin light chain kinase (autophosphorylation sites) - rak C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus C;Species: Oryctolagus cuniculus C;Species: Oryctolagus C;Spec	on sites) - ra 1997 ase.
A; Experimental source: skeletal muscle A; Note: sequence extracted from NCBI backbone (NCBIP:109204) C; Keywords: calmodulin binding Query Match 23.1%; Score 31; DB 2; Length 20; Best Local Similarity 37.5%; Pred. No. 4.8e+02; Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps	.0 sdp
Qy 3 APGTFSNTTSSTDICR 18 . : : 	

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 2-13an-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C; Accession: B49048
R; Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A; Title: Limited heterogeneity of T cell receptor variable region gene usage in juven A; Reference number: A49048; MUID: 92387250
A; Accession: B49048
A; Accession: B49048
A; Status: preliminary; not compared with conceptual translation
A; Residues: 1-18 <SIO>

Query Match 22.4%; Score 30; DB 2; Length 18; Best Local Similarity 50.0%; Pred. No. 6e+02; Matches 5; Conservative 1; Mismatches 4; Indels A; Experimental source: patient EV, IL-2R+ synovial T-cells A;Note: sequence extracted from NCBI backbone (NCBIP:113264) C; Keywords: T-cell receptor

2 CAPGTFSNTT 11

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Gaps

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LX-1 tumor antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 18.0ct-1991 #sequence_revision 18-0ct-1991 #text_change 05-Jan-1996
C;Accession: A39269
R;Rosenbaum, L.C.; Neuwelt, E.A.; Van Tol, H.H.M.; Loh, Y.P.; Verbalis, J.G.; Hellstr Proc. Natl. Acad. Sci. U.S.A. 87, 9928-9932, 1990
A;Title: Expression of neurophysin-related precursor in cell membranes of a small-cel A;Reference number: A39269; MUID:91088624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S60565
R; Degram, B.M.; Morse, D.E.
A; Degram, B.M.; Morse, D.E.
A; Title: Identification of eight homeobox-containing transcripts expressed during lar
                                                                                                                                                                                                                                                                                                   C;Accession: I54351
R;Akli, S.; Chomel, J.C.; Lacorte, J.M.; Bachner, L.; Poenaru, A.; Poenaru, L.
Hum, Mol. Genet. 2, 61-67, 1993
A;Title: Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs patients. A;Reference number: I54351; MUID:93258352
A;Accession: I54351
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C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
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C;Species: Haliotis rufescens (California red abalone)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
                       Gaps
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                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 29; DB 2; Lei
52.6%; Pred. No. 9.4e+02;
Mismatches 7;
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Pred. No. 9.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Status: preliminary, translated from GB/EMBL/DDBJ
A)Molecule type: mRNA
A)Residues: 1-21 <RES>
  Pred. No. 7.76
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:120040; OMIM:272800
                                                                                                                                                                                                                                     gene HEXA protein - human (fragment)
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C; Superfamily: beta-hexosaminidase
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80.0%;
38.5%;
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Matches 10; Conserv
  Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A;Title: Comparison of four grass pollen species concerning their allergens of grass A;Reference number: S38288; MUID:94092339
A;Recession: S38292
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-16 <PET>
                                                                                                                                                                                                                                                                                  dominated by
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                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30K allergen - rye (fragment)
C;Species: Secale cereale (rye)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 07-May-1999
C;Accession: S38292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucagon-like peptide 1 - marbled electric ray (fragment)
C;Species: Torpedo marmorata (marbled electric ray)
C;Bate: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 21-Nov-1997
C;Accession: A60317
R;Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.
                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule: type: mRNA
A;Residues: 1-13 <LEHA
A;Cross-references: EMBL:235698; NID:g527487; PIDN:CAA84767.1; PID:g527488
C;Keywords: T-cell receptor
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C; Accession: S47381

R; Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A; Description: Human HLA-A0201 restricted recognition of influenza A is A; Reference number: S47355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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A/Title: A truncated glucagon-like peptide I from torpedo pancreas.
A/Teference number: A60317
A/Accession: A60317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 16;
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Pred. No. 7.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                         T-cell antigen receptor VJ junction beta chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 2; Le
Pred. No. 6.1e+02;
0; Mismatches 3;
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A.Residues: 1-17 <CON>
C.Superfamily: glucagon
C.Keywords: "duplication; pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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Best Local Similarity
Matches 6; Conserv
  Query Match
Best Local Similarity
Matches 5; Conserv
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7 PAAPGT 12
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Riott, K.H.; Becker, S.; Gordon, R.D.; Rueterjans, H.
FEBS Lett. 278, 160-166, 1991
A.?Title: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geo
A.?Title: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geo
A.?Title: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geo
A.?Contents: annotation; conformation by (1)H-NMR
B.Wakamatsu, K.; Kohda, D.; Hatanaka, H.; Lancelln, J.M.; Ishida, Y.; Oya, M.; Nakamu
B.Jochemisstry 31, 12577-12584, 1992
A.Title: Structure-activity relationships of mu-conotoxin GIIIA: structure determinat
A.;Contents: annotation; conformation by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24K antigen - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 11-Dec-1992 #text_change 18-Jun-1993
C;Accession: B60278
R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium bov A;Reference number: A60278; MUID:91147217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Sepvords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor C; Keywords: amidated carboxyl end; hydroxyproline; experimental F; 3.15, 4-20, 10-21/Disulfide bonds: #status experimental F; 6,7/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental F; 17/Modified site: 4-hydroxyproline (Pro) #status experimental F; 22/Modified site: amidated carboxyl end (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium vivax
                                         A;Title: Tertiary structure of conotoxin GIIIA in aqueous solution.
A;Reference number: A44659; MUID:91299744
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Plasmodium vivax
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Sep-1997
C;Accession: JN0263; S21344
R;Ray, P.; Sharma, Y.D.
Biochem. Biochem. Biophys. Res. Commun. 184, 668-672, 1992
A;Title: Molecular cloning and serological characterization of a new Plasmoc A;Reference number: JN0263; MUID:92246949
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Pred. No. 1.8e+03;
2; Mismatches 2;
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A)Cross-references: GB:X53681; NID:g10084; PID:g10085
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Pred. No. 1.8e+03;
0; Mismatches 5
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54.58;
               6908-6916, 1991
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity
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A; Residues: 1-15 <RAY>
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                   Biochemistry 30,
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A.Residues: 1-22 <SAT>
R.Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydlc
A.Title: Conus geographus toxins that discriminate between neuronal and muscle sodium of
A.Reference number: A2379; MUID:85261316
A.Accession: A2379
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-22 <CRU>
R.Kohda, D.; Lancelin, J.M.; Inagaki, F.; Wakamatsu, K.
Submitted to the Brookhaven Protein Data Bank, December 1992
A.Reference number: A51994; PDB:1TCG
A.Contents: annotation; conformation by (1)H-NMR, residues 1-22
R.Contents: A1994; PDB:1TCG
A.Contents: A1994; PDB:1TCG
A.Contents: No. Inagaki, F. Inaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Sato, S.; Nakamura, H.; Ohlzumi, Y.; Kobayashi, J.; Hirata, Y.
FEBS Lett. 155, 277-280, 1983
A;Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins from A;Reference number: A91309; MUID:83210170
A;Accession: A01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Vibrio sp.
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Datession: T48881
R;Xu, Y:; Zhang, Y:: Liang, Z.Y.; Van de Casteele, M.; Legrain, C.; Glansdorff, N. Microbiology 144, 1435-1441, 1998
A;Title: Aspartate carbamoyltransferase from a psychrophilic deep-sea bacterium, Vibrio
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C;Date: 14-Nov-1983 #seguence_revision 14-Nov-1983 #text_change 15-Sep-2000
C;Accession: A01786; A23579
A;Reference number: S60564; MUID:93372986
A;Accessión:6560565
A;Molecule type: mRNA
A;Residues: 1-23 <DEG>
A;Cross-references: EMBL:X79372; NID:g495110; PIDN:CAA55917.1; PID:g495111
C;Genetics:
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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N;Alternate names: geographutoxin I (GTX I); myotoxin I
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Pred. No. 1.4e+03;
2; Mismatches 1;
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Pred. No. 1.7e+03;
3; Mismatches 4.
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A;Accession: T48881
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain 2693
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41.7%;
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Best Local Similarity 41.7
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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LCRPRRI 11
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Cibate: 02-Jul-1996 #text_change 21-Jul-2000
Ciraceson: 154283
Ciraceson: 154283
RiRegis, S.; Carrozzo, R.; Filocamo, M.; Serra, G.; Mastropaolo, C.; Gatti, R.
Hum. Genet. 96, 23-235, 1995
A; Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infam
A; Reference number: 154283; MUID:95362256
A; Accession: 154283
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-20 <RES>
A; Cross-references: GB:S78735; NID:91037139; PIDN:AAB35013.1; PID:91037140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aspartylglycosaminuria - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: 13744
R;Park, H.; Vettese, M.B.; Fensom, A.H.; Fisher, K.J.; Aronson, N.N.
Biochem. J. 290, 735-741, 1993
A;Title: Cfaracterization of three alleles causing aspartylglycosaminuria: two from a Br A;Reforence number: 137144; MUID:93207523
A;Reforence number: 137144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Convulsant peptide - cone shell (Conus textile)
C;Species: Conus textile (cloth-of-gold cone)
C;Species: Conus textile (cloth-of-gold cone)
C;Bate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: A59048
R;Cruz, L.J.; Ramilo, C.A.; Corpuz, G.P.; Olivera, B.M.
Biol. Bull. 183, 159-164, 1992
A;Fitle: Conus peptides: phylogenetic range of biological activity.
A;Reference number: A59048
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-23 <CRU>
C;Keywords: amidated carboxyl end; neurotoxin; venom
F;23/Modified site: amidated carboxyl end (Pro) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%; Score 26; DB 2; Length 20; 44.4%; Pred. No. 2.3e+03; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 2; Length 23; Pred. No. 2.6e+03; 2; Mismatches 7; Indels
                              Indels
     Pred. No. 1.9e+03;
1; Mismatches 7;
                                                                                                                                                                                                                                                                       arylsulfatase A - human (fragment)
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.8%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CAPGTFSNTTSSTDICRP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : : ||| | 9 | CCPPAYCEASG----CRP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.4
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                 || |:
| APKTYKEELKGTD 13
                                                                                3 APGTFSNTTSSTD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 TSSTDICRP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::1 |||
1 SAHSDHCRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
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A59048
                                                                                                                                                                                                                     RESULT
154283
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1;
A;Residues: 1-22 <RES>
A;Cross-references: EMBL:X73071; NID:g312227; PIDN:CAA51529.1; PID:g312228
C;Genetics:
A;Gene: AGU
                                                                                                                                                     Gaps
                                                                                                                                                  . '
                                                                                                                 Length 22;
                                                                                                                                                  4; Indels
                                                                                                                Score 25.5; DB 2;
Pred. No. 2.9e+03;
); Mismatches 4;
                                                                                                                Query Match 19.0%;
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                  6 TFSNTTSSTDICRPHQIC 23
                                                                                                                                                                                                     |||| | | | | TESRRVS-----HHIC 15
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- 5

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February 12, 2002, 13:03:56; Search time 10.06 Seconds (without alignments) 83.826 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                     Run on:
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US-09-800-909-2_COPY_163_185 134 1 PCAPGTFSNTTSSTDICRPHQIC 23 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

1274 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01523 conus geogr	26 brassi	P56683 spodoptera	99		66	P01524 conus geogr									P01371 tremella me	P31720 rattus norv	P30254 manduca sex		P30255 spodoptera			P80263 solanum tub			P33027 salmonella	P24335 trimeresuru		24	21843	929	9917 pseudomo	P30253 manduca sex
SUMMARIES	D	CXM1_CONGE	AFP2_BRANA	CP23_SPOER	PAP2_SPOEX	PAP3_SPOEX	TKNA_ONCMY	CXM2_CONGE	CXM3_CONGE	LANM_STRMU	HBB2_UROHA	DCMM_PSECA	CXAB_CONPE	HELT_HELHO	PAP1_HELVI	PAP2_HELVI	TA10_TREME	C1QA_RAT	PAP2_MANSE	JHBP_BOMMO	PAP1_SPOEX	CXAA_CONPE	RS11_SALTY	NUO3_SOLTU	CXA1_CONER	PSBH_SYNVU	SETB_SALTY	TX12_TRIWA	MIFH_TRISP	UCRQ_EQUAR	MCT3_MOUSE	RL5_HALHA	DCMM_PSECH	PAP1_MANSE
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ð	ue. at	20.1	20.1		19.0					18.3	17.9	17.5	17.5	17.5	17.5	17.5	17.2	17.2	16.8	16.4	16.4	16.0	15.7	15.7	15.7	15.7	15.7	15.7	14.9	14.9	14.9	14.9	14.6	14.6
	ö	27	~	25.5	25.5		25	25	•	24.5	\sim	23.5	23.5	23.5	23.5	23.5	23	23	22.5	22	22	21.5	21	21	21	21	21	21	20	20	20		19.5	C. 6T
	Result No.	1	7	9	4	2	φ	7	æ	o.	10	11	12	13.	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	35	2,5

P15471 conus stria P38496 locusta mig P38496 locusta mig P611519 conus geogr P811083 pinus pinas Q44507 anabaena sp P21586 caretta car P86614 zea mays (m P1738 morganella P28502 hirudo medi P28879 conus stria P03063 staphylococ P81527 pasteurelia	
CXA1_CONST LMA1_LOCMI CAN1_CONGE HS11_PINPS NIS1_ANASO RKGG_CARCR UCO8_MAIZE URBZ_MORMO ITHB_HIRME LPRM_STAAU SODE_PASPI	
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4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

ALIGNMENTS

RESULTA OCCUMAL OCC
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GTWSGVCGNNNACK 22
                                                    CP23_SPOER
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           σ
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                                           RESULT
                                                                         Db
           g
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                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus (Rape).
Eukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.";
FEBS Lett. 316:233-240(1993).
-i- FUNCTION: POSSESSES ANTIFUNGAL ACTIVITY SENSITIVE TO INORGANIC
MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                           .
0
                                                                                  Sodium channel inhibitor; Hydroxylation; Amidation; Venom; 3D-structure.
                                                                                                                                                                                                                                      Length 22;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 1; Length 23;
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATIONS.
-!- SUBUNIT: FORMS OLIGOMERS IN ITS NATIVE STATE.
-!- SIBULARITY: BELONGS TO THE GAMMA-PUROTHIONIN FAMILY.
PIR: S28992; 238992.
HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
CYSTEINE-RICH ANTIFUNGAL PROTEIN 2 (AFP2) (FRAGMENT).
                                                                                                                                                                                                       F6CB02ADB359813C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A11D4A9E364F5735 CRC64;
                                                                                                                                                                                                                                      Score 27; DB 1; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                          23 AA.
                                                                                                                                        HYDROXYLATION
                                                                                                                                                 HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002118; Gamma-thionin.
ProDom; PD002594; Gamma-thionin; 1.
PROSITE; PS00940; GAMMA_THIONIN; PARTIAL.
                                                                                                                                                                        AMIDATION
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                     20.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 23
23 AA; 2467 MW;
                                                                                                                                                                                                       2568 MW;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                            17
22
16
16
21
                                        PDB; 1TCG; 31-JAN-94.
PDB; 1TCH; 31-JAN-94.
PDB; 1TCJ; 31-JAN-94.
PDB; 1TCK; 31-JAN-94.
                  PIR; A01786; MXKN1.
PIR; A23579; A23579.
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                       22 AA;
                                                                                                                                                                                                                                                                               17 CRPHQIC 23
                                                                                                                                                                                                                                                                                                   15 CKPQRCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                        AFP2_BRANA
P30226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fungicide.
                                                                                                                  DISULFID
DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
NON_TER
SEQUENCE
                                                                                                       DISULFID
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                MOD_RES
MOD_RES
MOD_RES
HELIX
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Matches
                                                                                                                                                                                                                                                                                                                                             AFP2_BRANA
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Heliothis virescens.;
J. Biol. Chem. 266:12873-12877(1991).
-!- FUNCTION: CADISES RAPID, RIGID PARALXSIS WHEN INJECTED INTO
-!- FUNCTION: CADISES RAPID, RIGID PARALXSIS WHEN INJECTED INTO
-!- FUNCTION: CADISES RAPID, RIGID PARALXSIS WHEN INJECTED INTO
--- FUNCTION: CADISES RAPID, RIGID PARALXSIS WHEN BE TO REDUCE
--- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
PIR; D39855; D39855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and identification of paralytic peptides from hemolymph of
the lepidopteran insects Manduca sexta, Spodoptera exigua, and
                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. InterPro; IPR003463; GBP_PSP. Pfam: PF02425; GBP_PSP; 1. DISULEID 7 19 BY SIMILARITY. SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spodoptera exigua (Beet armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L., Quistad G.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.5; DB 1;
Pred. No. 8.8e+02;
2; Mismatches 7;
                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CARDIOACTIVE PEPTIDE CAP23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
PARALYTIC PEPTIDE II (PP II).
 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AA.
                                                                                                              Spodoptera eridania (Southern armyworm).
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91302298; PubMed=2071576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CAPGTFSNTTSSTDICRP 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Hemolymph;
CP23_SPOER
P56683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAP2_SPOEX
P30256;
                                                                                                                                                                                                                          SEQUENCE
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0;

Gaps

; 0

6; Indels

4; Mismatches

4; Conservative

Matches

Local Similarity

us-09-800-909-2_copy_163_185.rsp

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NCBI_TaxID=6491;
                                                                                                                                                                                                                                                                                                         18 RPHQ 21
                                                                                                                                                                                                                                                                                                                                                                             CXM2_CONGE
P01524;
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         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       CXM2_CONGE
                                                                                                                                                                                                                                                                                                         QΥ
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                                                                                                                                                                                                                                                                                                                                                                 Tabolation and identification of paralytic peptides from hemolymph of the lepidopteran insects Manduca sexta, Spodoptera exigua, and Heliothia Virescens.".

J. Blod. Chem. 266:12873-12877(1991).

-!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYWHH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. PIR: B39855; E39855.

InterPro; IPR001463; GBP_PSP.

Pfam; PF02425; GBP_PSP; 1.
                                                                                              Gaps
                                                                                                                                                                                                                                                    Spodoptera exigua (Beet armyworm).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neotera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea: Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID-7107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota: Metazoa; Chordata: (rainata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                           TISSUE-Hemolymph;
BEDLINE-91302298; PubMed-2071576;
Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
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ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
                                                                                             Indels
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                                                                         Length
                               BY SIMILARITY.
0A96CB4600855AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
0A96CB5EB7D55AE0 CRC64;
                                                                      Score 25.5; DB 1;
Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.5; DB 1;
Pred. No. 8.8e+02;
                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
PARALYTIC PEPTIDE III (PP III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
SUBSTANCE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                          A
                                                                                             Mismatches
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                                                                                                                                                                                         PRT;
IPR003463; GBP_PSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.0%;
33.3%;
                                                                       19.0%;
ilarity 33.3%;
Conservative
                                19
2477 MW;
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AA; 2505 MW;
                                                                                                                2 CAPGTFSNTTSSTDICRP 19
                                                                                                                            | || : | |:|
7 CTPG-YORTADGR--CKP 21
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7 CTPG-YQRTADGR--CKP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
Interpto; IPR003463; GBP
Pfam; PF02425; GBP_PSP;
Hemolymph.
DISULFID 7 19
                                                                                                                                                                                       STANDARD;
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Best Local Similarity
                                                                       Query Match
Best Local Similarity
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AA;
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P28499;
                                         SEQUENCE
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                                                                                             Matches
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DR
FT
SO
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Jensen J., Conlon J.M.;
"Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.";
Eur. J. Biochem. 206:669-664(1992).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
-EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASOBILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=96280640; PubMed-8688418;
Hill J.M., Alewood P.F., Craik D.J.;
"Three-dimensional Solution structure of mu-conotoxin GIIIB, a specific blocker of skeletal muscle sodium channels.";
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21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MU-CONOTOXIN GIIIB (MYOTOXIN II) (GEOGRAPHUTOXIN II) (GTX-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cruz L.J., Gray W.R., Olivera B.M., Zelkus R.D., Kerr L., Yoshikami D., Moczydlowski E.; "Conus geographus toxins that discriminate between neuronal muscle sodium channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus geographus (Geography cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 25; DB 1; L4 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             PIR; $23307; $23307.

PIR; $23308; $23308.

InterPro; IPR003580; Protachykinin.

InterPro; IPR002040; Tachykinin; 1.

SMART; $M00202; TK; 1.
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TISSUE-Brain;
MEDLINE-92298992; PubMed-1376687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-83210170; PubMed-6852238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.7
Best Local Similarity 100.
Matchès 4; Conservative
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15 DICRPHQIC 23
                       | | | : |
DCCTPPKKC 10
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                                                                                                                                                        NCBI_TaxID=1309;
                                                                                                                                              Streptococcus
                                                                        LANM_STRMU
P80666;
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SEQUENCE
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                                                                                                                                                                                          Gaps
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Biochemistry 35:8824-8835(1996).
-!- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK
MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annu. Rev. Biochem. 57:665-700(1988).
-1- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85261316; PubMed=2410412; Cruz L.J., Gray W.R., Olivera B.M., Zelkus R.D., Kerr L., Yoshikami D., Moczydlowski E.; Conus geographus toxins that discriminate between neuronal and muscle sodium channels."; 288(1985).
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0
                                                   PDB; IGIB; 08-NOV-96.
Sodium channel inhibitor; Hydroxylation; Amidation; Venom;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusoa; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydroxylation; Amidation; Venom
                                                                                                                                                                       Score 25; DB 1; Length 22;
                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 22;
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                                                                                                                                           E50402BA93199E01 CRC64;
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Pred. No. 9.9e+02;
                                                                                                                                                                                Pred. No. 9.9e+02;
1; Mismatches 4
                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
MU-CONOTOXIN GIIIC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
                                                                                                                                                                                                                                                                        22 AA.
                                                                                                          HYDROXYLATION HYDROXYLATION
                                                                                                                            HYDROXYLATION
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BY SIMILARITY
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                                                                                                                                     AMIDATION
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                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                           Conus geographus (Geography cone)
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                                                                                                                                                                       18.78;
44.48;
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22
2553 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 44.4،
احد کری (Conservative
                                                                                                                                                                       Query Match 18.7
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; C23579; C23579.
HSSP; P01524; 1GIB.
                                   PIR; A01787; MXKN2.
PIR; B23579; B23579.
                                                                                                                                                                                                           15 DICRPHQIC 23
                                                                                                                                                                                                                          2 DCCTPPRKC 10
                                                                                                                                             22 AA;
                                                                                                                                                                                                                                                                                                                                              Neogastropoda; Co
NCBI_TaxID=6491;
                           CHANNELS.
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                                                                        3D-structure.
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P05482;
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SEQUENCE
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-MAY-1991 (Rel. 18, Last annotation update)
HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
Uromastyx hardwickii (Indian spiny-tailed lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- MASS SPECTROMETRY: MW-2270.29; MW_ERR-0.21; METHOD-ELECTROSPRAY.
-1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
Interpro; IPR001049; Gallidermin.
Pfam; PF02052, Gallidermin; 1.
                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHA (2,3-DIDEHYDROALANINE).
D-ABU (AMINOBUTYRIC ACID).
DHA (2,3-DIDEHYDROBUTYRINE).
ALA-S-ALA (LANTHIONINE).
ABU-S-ALA (BATA-WETHYLLANTHIONINE).
ALA-S-ALA (BATA-WETHYLLANTHIONINE).
                                                                                                                                                                                                                                                                                                                                STRAIN=NY266; 1.
MEDLINE=97379322; PubMed=9237644;
Mota-Meira M., Lacroix C., Lapointe G., Lavoie M.C.;
"Purification and structure of mutacin B-Ny266: a new lantibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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961C1480401F92CE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00323; GALLIDERMIN.
Antibiotic; Bacteriocin; Lantibiotic; Plasmid.
                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LANTIBIOTIC MUTACIN B-NY266.
22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             produced by Streptococcus mutans.";
FEBS Lett. 410:275-279(1997).
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MEDLINE-84029159; PubMed-6628672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P18992;
01-NOV-1990 (Rel. 16, Created)
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37.5%;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE PORES.
                                                                                                                                                                    Streptococcus mutans.
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Best Local Similarity
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MEDLINE-9942956; PubMed=10226369; MEDLINE-99942956; PubMed=10226369; Molfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M., Baldwin M.A., Burlingame A.L.; Indertification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PINA and alpha-PINB: further investigation of labile sulfo- and phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Sulfation; Venom; 3D-structure.

DISULFID 2 8 16
DISULFID 3 16
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MEDILINE-90560878; PubMed-1693019;
MOCHCA-MOTALES J., Martin B.M., Possani L.D.;
"Isolation and characterization of helothermine, a novel toxin from
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97444322; Pubmed-9298951;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Crystal structure at I.1-A resolution of alpha-conotoxin PnIB:
Comparison with alpha-conotoxins PnIA and GI.";
Blochemistry 36:11330(1997).
I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
SELECTIVE FOR VERTERRALE SKELETAL MUSCLE NACHR, THE CONUS
PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heloderma horridum horridum (Mexican beaded 11zard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                              TISSUE-Venom;
MEDLINE-94347719; PubMed-8068627;
Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D., Spira M.E., Zlotkin E.;
                                                                                                                                         "New mollusc-specific alpha-conotoxins block Aplysia neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.5; DB 1; Length 16; Pred. No. 1.2e+03;
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conídae; Conus.
NÇBI_TaxID=37335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
05310FF95ED86AF5 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULFATION.
                                                                                                                                                                                                                                                                                                                            spectrometry.";
J. Mass Spectrom. 34:447-454(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                       acetylcholine receptors.";
Biochemistry 33:9523-9529(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.5%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1643 MW;
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16
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Best Local Similarity
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16
16 AA;
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P46693;
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MOD_RES
SEQUENCE
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01-FEB-1991 (Rel. 17, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] MEDIUM CHAIN (EC 1.2.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- COFÁCTOR: MOLYBDENUM.
-i- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas carboxydovorans.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Oligotropha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
   Nagvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; Score 23.5; DB 1; Length 15; 36.8%; Pred. No. 1.1e+03;
                            "Characterization of hemoglobin from the lizard Uromastix hardwickii."; PERS Lett. 162:290-295(1983). PIR: A05305, A05305. InterPro; IPRO00971; Globin. PROSITE; PS01033; GLOBIN; PARTIAL.
                                                                                                                                                                                                                Score 24; DB 1; Length 19;
Pred. No. 1.2e+03;
2; Mismatches 5; Indels
                                                                                                                          Heme; Oxygen transport; Respiratory protein; Erythrocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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SEQUENCE 15 AA; 1779 MW; 82DD3BF93E739D63 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NAY-2000 (Rel. 39, Last annotation update)
ALPHA-CONOTOXIN PNIB.
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Best Local Similarity 41.7%;
Matches 5; Conservative
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NON_TER 15 15
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Best Local Similarity 36.8
Matches 7; Conservative
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3 GDFGNISSAAAI 14
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P50985;
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Quistad G.B.;
Quistad G.B.;
Isolation and identification of paralytic peptides from hemolymph of the lepidopteran insects Manduca sexta, Spodoptera exigua, and Heliothis virescens.";
J. Biol. Chem. 266:12873-12877(1991).
I- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
I- SIMILARITY: BELONGS TO THE GBP / PSPI / PARALYTIC PEPTIDE FAMILY.
PIR: F39855; F39855.
                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-PRADIXTIC PEPTIDE I (PP I)
Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Petrygota: Neoptera; Endopterygota, Lepidoptera; Glossata; Ditrysia;
Noctuoidea: Noctuidae, Heliothines; Heliothis.
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Heloderma horridum horridum (Mexican beaded lizard) venom.";
Toxicon 28:299-309(1990).
-!- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF
REAR LIMES AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
MIGHT BE A HYPOTHERMIC TOXIN.
-!- MISCELLANBOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA
AND A PI OF 68.
PIR; A34859; A34859.
                                                                                                                                                                                                  Τ;
                                                                                                                                                                      Score 23.5; DB 1; Length 20;
Pred. No. 1.5e+03;
1; Mismatches 8; Indels
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Pred. No. 1.7e+03;
2; Mismatches 7; Indels
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2236CB436D655AFA CRC64;
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20 AA; 2156 MW; 91D62B36F7B4F940 CRC64;
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Last sequence update)
Last annotation update)
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MEDLINE-91302298; PubMed-2071576;
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33.3%;
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2524 MW;
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7 CIPG-YMRTADGR--CKP 21
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(Rel. 25, 1
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23 AA;
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P30252;
01-APR-1993 (
01-APR-1993 (
15-JUL-1599 (
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P30251;
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PAP2_HELVI
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the lepidopteran insects Manduca sexta, Spodoptera exigua, and
Heliothis virescens.";
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PARALYTIC PEPTIDE II (PP II).
Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                             Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
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Job time: 168 sec
                                                                                                                                                                             TISSUE=Hemolymph;
MEDLINE=91302298; PubMed=2071576;
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Best Local Similarity 33.3%;
Matches 6; Conservative
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7 CIPG-YMRTADGR--CKP 21
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                                                                                                                                                                                                                                           Quistad G.B.;
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Perfect score:

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Ogqvd6 rattus sp.
Ogutt6 schizosacch
Ogurt1 filobasidie
P90716 beroe ovata
Oggex5 human immun
Oggex human immun
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Oggex homo saplen
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MEDLINE-96085162; PubMed-8521863;
SCHUILE S., Stoffel W.;
SCHUILE S., Stoffel W.;
SCHUILE S., Stoffel W.;
"UDP galactose.ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins.";
Eur. J. Biochem. 233:947-953(1995).
SEOUBNCE 15 AA; 1657 MW; 84474749A06BFFCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
01-UNN-2000 (TREMBLrel. 14, Last annotation update)
01.GODENDROCYTE-SPECIFIC UP-GALACTOSE:CERAMIDE GALACTOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q78505 PRELIMINARY; PRT; 20 AA.
Q78505;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLQSRSD (FLORIDA LOCAL CONTROL 01), PARTIAL ENV CDS, V5
REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.6%; Score 33; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.4e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                          Q9S923
Q78486
Q78507
Q78508
Q78509
Q9Y8F8
Q93046
O69142
Q9S8B9
Q9S8B9
                      Q9UR51
P90716
Q9QEX5
Q9QEX4
Q13726
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P97944
Q9TWC6
Q9UGN8
  PRELIMINARY;
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  090V5;
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01-MAY-2000 (
01-JUN-2000 (
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286611 human immun
226159 plasmodium
294747 canis famil
295885 lupinus alb
                                                                                         (without alignments)
152.852 Million cell updates/sec
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                                                                              February 12, 2002, 13:04:16; Search time 22.01 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 PCAPGTFSNTTSSTDICRPHQIC 23
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Maximum Match 100%
Listing first 45 summaries
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sp_unclassified:*
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sp_human:*
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sp_bacteria:*
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Match Length DB
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBRSF (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION (FRACMENT).
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MEDLINE-92271245; PubMed-1589796;
Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
EMBL; M92126; AAA44496.1; -.
                                                                                               MEDLINE=92271245; PubMed=1589796; MEDLINE=92271245; PubMed=1589796; Ou C.Y., Clessielski C.A., Myers G., Bandea C.I., Luo C.C., Caresielski C.A., Myers G., Bandea C.I., Luo C.C., Chorber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L., Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A., Curran J.W., Jaffe H.W.; "Molecular epidemiology of HIV transmission in a dental practice."; Science 256:1165-11711(1922).

EMBL; M92150; AAA44592.1; -.
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                                                                                                                                                                                                                                                                  22.4%; Score 30; DB 12; Length 20;
40.0%; Pred. No. 5.5e+02;
Live 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Zhang L.Q., Leigh-Brown A.J.; Zhang L.Q., Leigh-Brown A.J.; Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                            Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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20 AA; 2049 MW; F44F963A48755A07 CRC64;
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Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Matches 6; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                       SEQUENCE FROM N.A.

Lin H.J., Siwak E.B., Hollinger F.B.;

Lin H.J., Siwak E.B., Hollinger F.B.;

Mutation rate of human immunodeficiency virus type 1 genomic RNA deduced from long term culture of its biological clones.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

Embl. ARI78667; AAF04373.1;

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MEDLINE-9325832; PubMed-8490625;
Akli S., Chomel J.C., Lacorte J.M., Bachner L., Poenaru A.,
Poenaru L.;
"Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs
patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 12; Length 18; Pred. No. 7.1e+02; Aismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 29; DB 4; Length 21; 52.6%; Pred. No. 8.2e+02; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        E17BAC9DD31D9910 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                            Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11676;
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                                                                                                                   Human immunodeficiency virus type 1
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EMBL; S61298; AAD13927.1;
HSSP; P06865; 1QBC.
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Matches 6; Conservative
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5A (FLORIDA PATIENT B), PARTIAL ENV CDS, VS REGION
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPAR5A (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
(FRACMENT).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-9271245; PubMed-1589796;
MCLINE-9271245; PubMed-1589796;
MCCIV., Clesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Morber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
Molecular epidemiology of HIV transmission in a dental practice.";
Science 255:1165-1171(1992).
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Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
EMBL; M92123; AAA44493.1; -.
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 9.6e+02;
2; Mismatches 4;
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SEQUENCE 17 AA; 1649 MW;
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Best Local Similarity
Matches 5; Conserv
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5E (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 01, Last annotation update)
VIRAL SAMPLE FLPARSD (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
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MEDLINE-92271245; PubMed=1589796;
Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Economou A.N., Multie J.J., Schochetman G., Berkelman R.L.,
Economou A.N., Mitte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
EMBL; M92125; AAA44495.1; -.
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"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
EMBL: M92112; AAA44468.1; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92271245; PubMed-1589796; Ou C.Y., Classielski, C.A., Myers G., Bandea C.I., Luo C.C., Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L., Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
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Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses: Retrold viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 9.6e+02;
2; Mismatches 4;
     AA.
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     17
     PRT;
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45.5%;
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PRELIMINARY;
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Gaps

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Length 23; 1; Indels

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CC387AE7BDA6C44D CRC64;
                                                                 Score 28; DB 5; I
Pred. No. 1.3e+03;
2; Mismatches 1;
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                                                                  20.9%;
57.1%;
                              23
2793 MW;
         Pfam; PF00046; homeobox; 1.

NON_TER 1 1

NON_TER 23 23

SEQUENCE 23 AA; 2793 MW;
                                                                                    4; Conservative
                                                                                                                                                                         PRELIMINARY;
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                                                                          Best Local Similarity
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5 LCRPRRI 11
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                                                                                                                                                     RESULT 12
Q78379
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Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
NCBI_TaxID=6454;
          Length 17;
                                                                                                                                                                                                                                                                                                                                                        20.9%; Score 28; DB 5; Length 21; llarity 57.1%; Pred. No. 1.2e+03; Conservative 2; Mismatches 1; Indels
                             4; Indels
                                                                                                                                                                                                                                             Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U09939; AAA18629.1; -.
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Herdmania.
NCBI_TaxID=7733;
                                                                                                              Q25086 PRELIMINARY; PRT; 21 AA. Q25086; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CLONE AHOX4 HOMEOBOX PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                            21 AA; 2650 MW; AB7FF3AF1FA659C3 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HROX3 (FRAGMENT).
        20.9%; Score 28; DB 12;
45.5%; Pred. No. 9.6e+02;
iive 2; Mismatches 4;
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Pfam; PF00046; homeobox; 1.
Homeobox; DNA-binding; Nuclear protein.
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MEDLINE=93372986; Pubmed=7689904;
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Query Match
Best Local Similarity
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                                               NTTSSTDICRP 19
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5C (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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SEQUENCE FROM N.A.

MEDLINE-92271245; PubMed=1589796;

OU C.Y., Clesielski C.A., Myers G., Bandea C.I., Luo C.C.,

Korber B.T., M., Mullins J.I., Schochetman G., Berkelman R.L.,

Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,

Curran J.W., Jaffe H.W.;

"Molecular epidemiology of HIV transmission in a dental practice.";

EMBL, M92124; AAA44494.1;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=79682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.1%; Score 27; DB 12; Length 17; 45.5%; Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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NON_TER 17 17
SEQUENCE 17 AA: 1652 MW; 34757BBFD1240170 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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2; Mismatches 4
17 AA.
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Gaps

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Length 22;

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Score 27; DB 13; Length 22
Pred. No. 1.7e+03;
3; Mismatches 1; Indels
                                                                        AE4485CB7FF7CF1D CRC64;
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                         Homeobox; Nuclear protein; DNA-binding
                                                                                                                      20.1%;
42.9%;
                                                                       22 AA; 2703 MW;
           Pfam; PF00046; homeobox; 1.
                                                                                                                                           Best Local Similarity 42.9
Matches 3; Conservative
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2 LCRPRRV 8
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MOX-B3-LIKE HOMEODOMAIN PROTEIN (FRAGMENT).
MOXONG SAXAELIIS (Striped bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
MOXONIGAE; Moxond.
NCBI_TAXID-34816;
bacterium, Vibrio strain 2693: properties of the enzyme, genetic organization and synthesis in Escherichia coll."; Microbiology 144.1435-1441(1998). EMBL: Y09786; CAA7022.1; - SEQUENCE 20 AA; 2241'MW; 35C31F588FBB5D63 CRC64;
                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PNV2 TOXIN (FRAGMENT).
PNV2 TOXIN (FRAGMENT).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.

MEDLINE-94030062; PubMed-8216354;

Bento A.C., Novello J.C., Marangoni S., Antunes E., Giglio J.R., Oliveira B., de Nucci G.;

Oliveira B., de Nucci G.;

Tidentification of a new vascular smooth muscle contracting polypeptide in Phoneutria nigriventer spider venom.";

Blochem. Pharmacol. 46:1092-1095(1993).

SEQUENCE 20 AA; 2176 MW; F28C3D81D983BCA5 CRC64;
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"Survey of Hox-like genes in the teleost Morone saxatilis:
"implications for evolution of the Hox gene family.";
Mol. Mar. Biol. Biotechnol. 3:149-157(1994).
EMBL; U09944; AAC59650.1; -.
HSSP; P02833; 9ANT.
                                                                                                                      20.1%; Score 27; DB 2; Length 20; 41.7%; Pred. No. 1.6e+03; Live 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                          20 AA.
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MEDLINE-95005122; PubMed-7921046;
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                                                                                                                      Query Match 20.1
Best Local Similarity 41.7
Matches 5; Conservative
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6 DICQP 10
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R1 and R2 peptide
R2 peptide
R3 and R4 peptide
R4 and R5 Peptide
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Peptide #19 for ep
Antigenic peptide
Human delta3 fragm
TGF beta 2 mutant
Erythropoletin rec
R1 and R2 peptide
R1 and R2 peptide
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Fibronectin-like s
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Immunopeptide deri
Hepattis C virus
HCV E2 peptide
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R1 and R2 peptide
Peptide #1456 enco
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Pharmaceutically a
Human umbilical co
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Rl and R2
Human APC
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                                AAY20893
AAU05335
AAU05356
AAU05356
AAU05359
AAU05399
AAW06235
AAW06235
AAW06235
AAW06235
AAW06235
AAW14391
AAY14391
AAY14391
AAY14391
AAY16393
AAV06323
AAV06339
AAV06339
AAV06339
AAV06339
AAV06360
AAR84512
AAV06360
AAR84512
AAV06360
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AAV06360
AAR84512
AAV06360
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970S-0045689.
970S-0045739.
970S-0045780.
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WO9850074-A2
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06-MAY-1997;
06-MAY-1997;
06-MAY-1997;
06-MAY-1997;
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18-FEB-1998;
18-FEB-1998;
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AAW95323
Costant and variab
P. pastoris 1ysyl
P. pastoris 1ysyl
YadA homologous pe
Human secreted pro
RI and R2 peptide
RI and R2 peptide
RI and R2 peptide
RI and R2 peptide
R1 and R2 peptide
R1 and R2 peptide
R1 and R2 peptide
                                                                                                                        February 12, 2002, 13:00:40 ; Search time 23.63 Seconds
(without alignments)
72.098 Million cell updates/sec
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/ Sides/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/ Sides/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY51961
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Gapop 10.0 , Gapext 0.5
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Query Match

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Minimum DB seq length: 0 Maximum DB seq length: 23

Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Klingler J,

Lueddecke E,

for formulation

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This invention describes a novel method to manufacture a preparation of an active substance, where the active substance is surrounded by at least one layer consisting of a protein that is cross-linked by an enzyme chosen from the group of lipoxygenase, protein disulfide calculated by an disulfide reductase, throsine oxidase or sulfhydryl oxidases. Enzymes chosen from lipoxygenase, protein disulfide reductase, protein disulfide reductase, tyrosine oxidase and peroxidase, protein disulfide reductase, tyrosine oxidase and peroxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases, especially lysyl oxidase are useful for formulation of preparations of active substances. The method of the invention is preparations are useful as food additives or fodder or as pharmaceuticals. AAY51951-Y51962 represent fragments of the Pichia formulation are useful as food additives or fodder or as paramaceuticals. AAY51951-Y51962 represent fragments of the pichia formulation are used to illustrate the method of the
                                                                                                                                                                                            which surrounds the active substance with an enzyme, especially a novel
                                                                                                                                                                        Manufacture of active preparations comprises cross linking a protein,
                                                                                                                                                                                                                           lysyl oxidase from Pichia pastoris
                                                                                                                                                                                                                                                                          Claim 17; Page 17; 22pp; German.
                                                                         Friedrich T, Bewert W,
                                                                                                                        WPI; 2000-257743/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AA;
                         (BADI ) BASF AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lysys oxidase; lipoxygenase; protein disulfide isomerase; phenol oxidase; peroxidase; protein disulfide reductase; tyrosine oxidase; fodder; sulfhydryl oxidase; food additives.
                                                                                                                                                                                                                                                                                                                                    Chlamydia species. The invention provides a composition that comprises at least two agents, where each of the agents is effective against a different phase of the chlamydial life cycle. The agents are selected from: (a) agents targetted against cryptic phase of chlamydial life cycle; (b) agents targetted against cryptic phase of chlamydial life cycle; (c) agents targetted against replicating phase of chlamydial life cycle; (d) probenicid, and (e) antiporphyric acid. The composition an animal or human and is applied until the animal or human tests megative for chlamydia infection. It is also used to treat biological material infected with Chlamydial Diagnostic kits for antibody assays against recombinant major outer membrane protein (MOMP), and for DNA amplification assays for chlamydial genes, are used to diagnose disease,
                                                                                                                                                                                                                                                                                                                   The invention relates to the diagnosis and management of infections by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                             Composition with two agents effective against different stages of chlamydial life cycle - comprises agent targetted against cryptic phase, against elementary body phase, against replicating phase, probenicid and antiporphyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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    P. pastoris lysyl oxidase peptide fragment #11.

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Pred. No. 5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51961 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                     Claim 4; Fig 3; 138pp; English.
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                                               Stratton CW;
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Best Local Similarity 64.3-
Conservative
(UYVA-) UNIV VANDERBILT.
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                                                                                             WPI; 1999-059653/05
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                                               Mitchell WM,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Lysyl oxidase; lipoxygenase; protein disulfide isomerase; phenol oxidase; peroxidase; protein disulfide reductase; tyrosine oxidase; food;
                                               Gaps
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Score 41; DB 21; Length 17; Pred. No. 25; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klingler J,
                                                                                                                                                                                                                                                                                                                                                                        P. pastoris lysyl oxidase fragment #11
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                                                                                                                                                                                                                                          AAY51973 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulfhydryl oxidase; animal feed.
30.6%;
70.0%;
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                                                 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-272257/24
                                                                                          1 PCAPGTFSNT 10
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7 pcapgvvynt 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pichia pastoris.
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the polypeptides in a suitable culture system. The composition can be used to vaccinate a patient against a proteobacterial infection.
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                                                                                                                      Similarity
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30-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                               AAW73416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to peptides AAB51512 - AAB51537 which represent conserved proteobacterial extracellular domains. Sequences AAB51538 - AAB51618 represent peptides homologous to YadA, a yersinia adhesin which is an important virulence determinant of the Yersinia species. The invention includes an antibody which binds to the proteobacterial extracellular peptides, and an immunogenic composition containing the antibody used as a vaccine to prevent infection by a proteobacteria. The polypeptides and antibodies are useful in the treatment and prevention of proteobacterial infections. The polypeptides can also be used to identify compounds which antagonize the binding of a bacterial adhesion to its ligand. The host cell can be used to produce
                                                                               from lipoxygenases, protein disulfide isomerases, phenol oxidases and peroxidases, lysyl oxidases, protein disulfide isomerases, tyrosine oxidases or sulfihydryl oxidases is used to formulate compositions containing active ingredients. (I) is useful for crosslinking protein layers surrounding active ingredients in food, animal feed and pharmaceutical products. The compositions can be formulated without using chemical crosslinking agents. AAY51963-Y51974 represent fragments of the Pichia pastoris lysyl oxidase protein which is used to
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
                                                                   invention describes a novel method where an enzyme (I) selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; extracellular domain; virulence determinant; YadA; adhesin; proteobacterial infection prevention; vaccine.
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                                                                                                                                                                                                                                                                                                             DB 21; Length 17;
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                                                                                                                                                                                                                                                                                                                                               3,
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                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 59; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB51542 standard; Peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                 Claim 17; Page 16; 20pp; German.
                                                                                                                                                                                                                                                                                                             30.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-2000; 2000WO-US09866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YadA homologous peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                           Query Match 30.6
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 1 PCAPGTFSNT 10
                                                                                                                                                                                                                                                                                                                                                                                                               7 pcapgvvynt 16
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 ingredients
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                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia, hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. cancers, neurological disorders, immune diseases, developmental disorders or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is encoded by a cDNA of the invention, designated
                                                                           .;
2
                         Length 22;
Score 37; DB 21; Length 22
Pred No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein encoded by Gene No. 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endress GA, Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 157; 188pp; English.
                                                                                                                                                                                                                                                                                                   AAW73416 standard; Protein; 23 AA
                                                                         Ξ.
                      27.6%;
50.0%;
                                                                                                                                                       97US-0048190.
97US-0048356.
97US-0050935.
97US-0056250.
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                                                                                                                            3 APGTFSNTTSSTDICRPHQI 22
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97US-0044039
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97US-0048101
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                           10; Conservative
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and for boosting the red blood count of a patient prior to surgery.

AĄ;

17

Sequence

S X C

Length 17;

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can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer.
                                                                                         tumours, neurological disorders, in analysis of treatment of cancer, deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence for potential R1 and R2 peptide #4 can be used to form a peptide dimer that binds and activates the erythropoietin receptor (BPO-R). Various possible peptide sequences for R1 and R2 (AAMU05301-AAU0539) are described in the present invention. Also described is method for synthesising such peptide dimers which act as EPO-R agonists. The method is useful for synthesising peptide dimers which are useful, in vitro, as tools for understanding the biological role of EPO, in the development of other compounds that bind to SPO-R, as commercial research reagents for various medical research and diagnostic applications, for detecting EPO receptors on living cells, for treatment of disorders associated with a deficiency of EPO, such as end-stage renal failure/dialysis, anaemia associated with AIDS and chroatc inflammatory diseases, autoimmune diseases and malignancies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthesizing peptide dimer useful as erythropoietin receptor agonist by binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments -
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
renal failure; anaemia; chronic inflammatory disease;
autoimmune disease; malignancy; red blood count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R1 and R2 peptide #4 useful as erythropoietin receptor agonist.
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0
                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                           Score 37; DB 20;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU05310 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2-5; Fig 1; 43pp; English.
                                                                                                                                                                                                                                                                                                         27.6%; 43.8%;
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                                                                                                                                                                                                                                                                                                                              Local Similarity 43.8
les 7; Conservative
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                                                                                                                                                                                                                                                 23 AA;
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                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthesizing peptide dimer useful as erythropoletin receptor agonist by binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence for potential R1 and R2 peptide #3 can be used to form a peptide dimer that binds and activates the erythropoletin receptor (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-AAU05393) are described in the present invention. Also described is a method for synthesising such peptide dimers which act as EPO-R agonists. The method is useful for synthesising peptide dimers which are useful, in vitro, as tools for understanding the biological role of EPO, in the development of other compounds that bind to EPO-R, as commercial research reagents for various medical research and diagnostic applications, for detecting EPO receptors on living cells, for treatment of disorders associated with a deficiency of EPO, such as end-stage renal failure/dialysis, anaemia associated with AIDS
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                    Human, erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
renal failure; anaemia; chronic inflammatory disease;
autoimmune disease; malignancy; red blood count.
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                                                                                                                                                                                                                                                                                       R1 and R2 peptide #3 useful as erythropoletin receptor agonist.
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                                Indels
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Pred. No. 2.2e+02;
1; Mismatches 4;
Score 34.5; DB 22
Pred. No. 2.1e+02;
; Mismatches 4
                                                                                                                                                                                   AAU05309 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2-5; Fig 1; 43pp; English.
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25.7%;
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Best Local Similarity 43.87

-Local 7; Conservative
Query Match 25.7
Best Local Similarity 43.8
Matches 7; Conservative
                                                                   5 GTFS-NTTSSTDICRP 19
                                                                                    ||:|: |::|||
| gtyschfgpltbvcrp 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                     AAU05309;
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                                                                                                                                                                   AAU05309
ID AAU0
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EPO deficiency;

AAU05307;

AAU05307

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The present sequence for potential R1 and R2 peptide #9 can be used to form a peptide dimer that binds and activates the erythropotetin receptor (EPO-R). Various possible peptide sequences for R1 and R2 receptor (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-AAU05303) are described in the present invention. Also described is a method for synthesising such peptide dimers which are useful, in vitro, as useful for synthesising peptide dimers which are useful, in vitro, as tools for understanding the biological role of EPO, in the development of other compounds that bind to EPO-R, as commercial research reagents for various medical research and diagnostic applications, for detecting EPO receptors on 114ing cells, for treatment of disorders associated with a deficiency of EPO, such as end-stage renal failure/dialysis, anaemia associated with AIDS and chronic inflammatory diseases, autoimmune diseases and malignancies, and for boosting the red blood count of a patient prior to surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthesizing peptide dimer useful as erythropoietin receptor agonist binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; erythropoletin receptor; EPO-R; EPO agonist; EPO deficiency; renal failure; anaemia; chronic inflammatory disease; autoimmune disease; malignancy; red blood count.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R1 and R2 peptide #2 useful as erythropoietin receptor agonist.
                                            Rl and R2 peptide #9 useful as erythropoletin receptor agonist.
                                                                                     Human; erythropoietin receptor; EPO-R; EPO agonist; El
renal failure; anaemia; chronic inflammatory disease;
autoimmune disease; malignancy; red blood count.
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Pred. No. 2.5e+02;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU05308 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%;
                                                                                                                                                                                                                                                                                                                       24-NOV-2000; 2000WO-US32224
                                                                                                                                                                                                                                                                                                                                                                    99US-0449064
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24-OCT-2001 (first entry)
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Best Local Similarity 43.00
Best Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-417749/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AA;
                                                                                                                                                                                                                             WO200138342-A2
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU05308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthesizing peptide dimer useful as erythropoietin receptor agonist by binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                     Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
renal failure; anaemia; chronic inflammatory disease;
autoimmune disease; malignancy; red blood count.
                                                                                                                                                                                                                                                                          R1 and R2 peptide #1 useful as erythropoietin receptor agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.5; DB 22;
Pred. No. 2.5e+02;
4; Mismatches 4;
                                                                                                                                    20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU05315 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.7%;
                                                                                                                                    AAU05307 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-2000; 2000WO-US32224
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Li: |: |::||| 2 gtyschfgpltbvcrp 17
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Best Local Similarity
Matches 7; Conserv
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Balu P;

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Gaps

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AAU05315;

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RESULT AAU05315

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Sequence

Length 20; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence for potential R1 and R2 peptide #2 can be used to form a peptide dimer that binds and activates the erythropoietin receptor (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-AAU05393) are described in the present invention. Also described is a method for synthesising uch peptide dimers which act as EPO-R agonists. The method is useful for synthesising peptide dimers which are useful, in vitro, as tools for understanding the biological role of EPO, in the development of other compounds that bind to EPO-R, as commercial research reagents for various medical research and diagnostic applications, for detecting EPO receptors on living and diagnostic applications, for detecting EPO receptors on living such as end-stage renal failure/dialysis, anaemia associated with AIDS and chronic inflammatory diseases, autoimmune diseases and malignancies, and for boosting the red blood count of a patient prior to surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                             Synthesizing peptide dimer useful as erythropoietin receptor agonist by binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 22; Length 21;
Pred. No. 2.6e+02;
1; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annexin V; hepatitis B surface antigen; immunogen; vaccine; hepatitis delta virus; infection; HBsAg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B surface antigen derived peptide (IGP 1082)
                                                                                                                                                                                                                                                                                                                                                                                    Example 10-12; Fig 1; 43pp; English.
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43.8%;
                                                                                  24-NOV-2000; 2000WO-US32224
                                                                                                                            99US-0449064
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96EP-0870164.
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Best Local Similarity 43.8'
'. Conservative
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                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD.
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Hepatitis b virus.
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WO200138342-A2.
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                                                                                                                            24-NOV-1999;
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                                             31-MAY-2001.
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The invention relates to an immunogenic peptide derived from hepatitis B surface antigen (HBsAg) which competes with the hepatitis B surface antigen/annexin V interaction or which binds a compound or antibody competing with the hepatitis B surface antigen/annexin V interaction.

Also claimed are: (1) a combination of the immunogenic peptide and a negatively charged phospholipid; (2) a peptide composition comprising the immunogenic peptide; (3) a vaccine composition comprising the immunogenic peptide as an active substance; (4) antibodies which specifically bind to the peptide and inhibit binding of HBsAg to annexin V, and (5) a therapeutic composition comprising as an active substance the antibodies of (4).

The vaccine of (3), and the therapeutic composition of (5), can be used as an innoculum to vaccinate humans against an infection with hepatitis B and/or hepatitis Delta virus The immunogenic peptide can be used in a method to detect antibodies which are capable of competing with the hepatitis B and/or hepatitis Delta virus surface antigen/annexin V interaction. The immunogenic peptide can also be used to screen for interaction. The immunogenic peptide can also be used to screen for drugs which block the binding between annexin V and the peptide, and as a therapeutic to treat humans infected with hepatitis B virus and/or hepatitis Delta virus. The present sequence represents one of the peptide fragments derived from HBsAg which were synthesised to map the
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                                                                                                                            Immunogenic polypeptide from hepatitis B surface antigen - useful
in, e.g. vaccine against hepatitis B virus or hepatitis delta virus
infection
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renal failure; anaemia; chronic inflammatory disease;
autoimmune disease; malignancy; red blood count.
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    Yap
    Maertens G,
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                                                                                                                                                                                                                                                                                                                                 Example 3; Page 35; 71pp; English.
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Depla E,
                                                                                 WPI; 1998-388040/33.
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Matches 8; Conserv
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В;

Vogelstein

Nakamura Y,

Thliveris A,

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White RL,
 Albertsen H,
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            Hedge PJ;
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                                                                                          The present sequence for potential R1 and R2 peptide #47 can be used to form a peptide dimer that binds and activates the erythropoletin receptor (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-AAU05303) are described in the present invention. Also described is a method for synthesising such peptide dimers which are useful. The method is useful for synthesising peptide dimers which are useful, in vitro, as tools for understanding the biological role of EPO, in the development of other compounds that bind to EPO-R, as commercial research reagents for various medical research and diagnostic applications, for detecting EPO receptors on living cells, for treatment of disorders associated with a deficiency of EPO, such as end-stage renal failure/dialysis, anaemia associated with AIDS and chronic inflammatory diseases, autoimmune diseases and malignancies, and for boosting the red blood count of a patient prior to surgery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APC gene; Adenomatous Polyposis Coli gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumour; adenoma; carcinoma; cancer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; repeat region.
                       Synthesizing peptide dimer useful as erythropoietin receptor agonist by binding linking group with functional groups as initiation sites for peptide synthesis to support and synthesizing peptide segments .
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human APC protein 20 aa repeat #4 (1643-1662).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB23019 standard; peptide; 20 AA.
                                                                      Disclosure; Fig 1; 43pp; English.
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(UYJO ) UNIV JOHNS HOPKINS.
(UTAH ) UNIV UTAH.
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91GB-0000963.
91GB-0000974.
91GB-0000975.
91US-0741940.
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                                                                                                                                                                                                                                                                                                                                       4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CANC-) CANCER INST.
WPI; 2001-417749/44
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Matches 4; Conserv
                                                                                                                                                                                                                                                                            20 AA;
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tbvcrpn 18
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                                                                                                                                                                                                                                                                             Sequence
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Polyposis Coli (APC) protein in a sample. The method involves contacting the sample with antibodies which specifically binds to the contacting the sample with antibodies which specifically binds to the protein, and detecting an APC-antibody complex. Mutations in the APC protein, and detecting an APC-antibody complex. Mutations in the APC gene play a role in tumorigenesis, indicating that it is a tumour suppressor gene. It is located on chromosome 5q21, which corresponds to the FAP (familial adenomatous polyposis) locus. FAP is an autosomal dominant inherited disease in which affected individuals develop hundreds to thousands of adenomatous polyps in the colon and rectum, some of which progress to malignancy. The FAP locus is often found to be deleted in sporadic (i.e., non-familial) adenomas and carcinomas, and chromosome 5g deletions have also been observed in tumours of the lung, breast, colon, rectum, bladder, liver, sarcomas, stomach, and prostate, and in leukaemias and lymphomas. Although the FAP locus contains several other genes such as FER, FER, TER, TER, and APC, it is thought that mutations in the APC gene play a key role in the development of FAP and sporadic tumours. The method is useful for detecting appropriation to progress in mour sample. The method is useful for diagnosing or prognosing negative for detecting a genetic prediagosition to progress to the method is useful for diagnosing or prognosing negative for detecting a genetic prediagosition to progress to the progress of t
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                                                                                                               Detecting Adenomatous Polyposis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that specifically bind to APC protein and detecting the complex formed -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a novel method for detecting Adenomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that are semiregularly spaced in the human APC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human presentlin I mutant protein fragment 39.
                                                                                                                                                                                                                                                                                                                                                               Example 15; Column 33-34; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY20893 standard; Protein; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 cvegtpinfstats1sdl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CAPGT --- FSNTTSSTDI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4
Matches 8; Conservative
WPI; 2000-565003/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
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                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, sepecially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, alzoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, allows a definitive diagnosis of Alzheimer's disease in living patients, and many others listed or the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, envofilament-F, presentlin 1, presentlin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lumphoma 2 (bc1-2) proto-oncogene, semaphorin III, HUPF-I, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                        Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dextranase; thermostable enzyme; dextran hydrolysis; sugar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 19; Length 15;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                        Grosveld FG, Van Leeuwen FW;
                                                                                                               RIJKSUNIV UTRECHT.
ROYAL NETHERLANDS ACAD ARTS & SCI
                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 10; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75932 standard; Protein; 16 AA.
                                                                                                                                            UNIV ROTTERDAM ERASMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dextranase N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penicillium minioluteum HI-4
                                                       98WO-IB00705
                                                                                97US-0043163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.6
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                 WPI; 1998-609901/51.
N-PSDB; AAX75761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA;
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                                                                                                                                                                       Burbach JPH,
                                                       02-APR-1998;
                                                                                   10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||||
|4 ccpgtf |
                           15-0CT-1998,
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                                                                                                             UYUT-)
                                                                                                                                            UYRO-)
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The N-terminal region of P. minioluteum dextranase was sequenced using the Edian degradation method. Dextranase may be secreted as a recombinant protein by the transformed host, Pichia pastoris. The recombinant enzyme has higher thermal stability than the natural P. minioluteum enzyme (specifically an optimum temp. of 55-60 deg and a half-life of 7.6 hr at 50 deg), and it can be used in the sugar industry for sugarcane juice dextran hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                    Delgado Boada JM, Campana HR, Curbelo DM, Jimenez ER;
Barton CF, Cremata Alvarez JA, Garcia Fernandez R;
Garcia Garcia BM, Gonzalez Martinez ME, Herrera Martinez LS;
Margollez Clark E, Morera Cordova V, Raices Perez-Castaneda MR;
                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence encoding Penicillin minioluteum dextranase useful for the high-level industrial prodn. of dextranase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 16;
Pred. No. 3.1e+02;
1; Mismatches 6;
                                                                                                            (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: February 12, 2002, 13:03:52 Job time: 192 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 7; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%;
46.2%;
94EP-0203614.
                                                       93CU-0000115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFSNTTSSTDIC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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Best Local Similarity
'hae 6; Conserve
                                                                                                                                                                                                                                                                                                                 WPI; 1995-247530/33.
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gttnnthcgadfc
                                                       14-DEC-1993;
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Tue Feb 12 15:03:45 2002

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Appl Appl Appl

Appli Appli Appli App11

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APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                      sednence sed
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; Length 15;
Pred. No. 0.00083;
0; Mismatches 1; Indels
US-08-612-973-83
US-08-927-597-83
US-08-323-531-8
US-08-107-794A-8
PCT-US93-07424-8
PCT-US95-02087-8
US-08-484-635-244
US-08-827-570-244
US-08-827-570-244
US-08-827-570-244
US-08-827-770-244
US-08-877-763-7
US-08-61-488-80-14
US-08-62-999A-280
US-08-62-999A-280
US-08-62-999A-315
PCT-US95-04018-49
                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/221,583 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-221-583-45
Sequence 45, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-221-583-45
     5 GTFSNTTSSTDICRP 19
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     COUNTRY: US
ZIP: 19403
   Query Match
     RESULT
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Sequence 46, Appl
Sequence 44, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 24, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 44, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
                                                                                                                                                   (without alignments)
41.572 Million cell updates/sec
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Patent No. 5217891
Sequence 78, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 178, Sequence 63, Al Sequence 649,
                                                                                                                              February 12, 2002, 13:02:40; Search time 12.45 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-221-583-45

US-08-221-583-46

US-08-221-583-46

US-08-221-583-44

US-08-221-583-44

US-08-221-583-47

US-08-221-583-47

US-08-221-583-47

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US-08-221-583-47

US-08-221-583-48
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US-09-101-146-58
US-08-34-618-3
US-08-934-915-141
US-08-693-092-4
US-08-508-836A-4
US-08-629-001A-4
US-08-652-127-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-318-193-63
US-09-461-697-449
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US-08-484-635-178
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US-08-827-570-178
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                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                 US-09-800-909-2_COPY_163_185
134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 23
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                                                                                                                                                                                                                                                                                Scoring table:
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Maximum DB
                                                                                            OM protein
                                                                                                                                                                                                                                            Sequence:
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Gaps

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Length 15;
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APPLICANT: Kruszynski, Marian
APPLICANT: Meric, Miljenko
APPLICANT: Meber, Robert W.
TITLE OP INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 5; 1
Pred. No. 0.00083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                      PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 5.1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-ARR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/221,581 FILING DATE: 01-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4

PCT-US95-04018-46

Sequence 46, Application PC/TUS9504018

Sequenck INFORMATION:
APPLICANT: Heavner, George A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEUTER REALDARD TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        : 15 amino acids amino acid
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide
PCT-US95-04018-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GTFSNTTSSTDICRP 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                 Sequence 46, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STRRET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One Liberty Place 46th Floor
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COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.7
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                  ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNTTSSTDIARPHQI 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SNTTSSTDICRPHQI 22
                                                                                                                                                                                                                                         STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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US-08-221-583-46
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Sequence 47, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.0%; Score 71; DB 5; Length 15; 100.0%; Pred. No. 0.0011; Live 0; Mismatches 0; Indels
                                                                                                                                                                    TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prea ...
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CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: DELUCA: MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CCOR-0232 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEPAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
                                              Sequence 44, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: WordPerfect 5.1
                                                                                    APPLICANT: Heavner, George A. APPLICANT: Kruszynski, Marian APPLICANT: Mervic, Miljenko APPLICANT: Weber, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,229
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         19403
        RESULT 6
PCT-US95-04018-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
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...a 0; Indels
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Pred. No. 0.00083;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Debuca. Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
NAME; Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-349
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               53.7%;
93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-46
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CITY: Philadelphia
STATE: Pennsylvania
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CLASSIFICATION: 514
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Best Local Similarity
Matches 14; Conserv
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US-08-221-583-44
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US-08-221-583-44
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EXPRESSION OF THE RECOMBINANT TUMOR NECROSIS FACTOR BINDING PROTEIN I (TBP-I): 26
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USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 25.618
                                                                                                                                                                                                                                                                                                                                          Score 57; DB 5;
Pred. No. 0.082;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
RELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-310
TELEPRAX: (215) 568-310
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-126-016-24
; Sequence 24, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
APPLICANT: WALLACH, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADERRA, DAN
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: NECROSIS FA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                          Query Match 42.5%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOPHAR, YARON
KEMPER, OLIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 amino acids
                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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STRANDEDNESS: si
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0
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 1; Length 15; Pred. No. 0.082; 0; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Mervic, Miljenko
APPLICANT: Meber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DebLOGA, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORTGPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04018 FILING DATE:
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APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-08-221-583-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Pennsylvania
      Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 TSSTDICRPHQI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                     FILING DATE:
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One Liberty Place 46th Floor
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88.9%;
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Best Local Similarity 88.3v.
S.hoq 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide PCT-US95-04018-48
                                                                                     ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                      Pennsylvania
                 STREET: One Liberta
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION:
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   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POPOLOGY:
                                                                                                                                                                          SOFTWARE:
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                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
UMBRE NO ESQUEANCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
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CURRENT AAPLICATION DATA:
PPLICATION NUMBER: US/08/221,583
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.8%; .Score 44; DB 1; Length 15; 88.9%; Pred. No. 4.3;
                                                  35.8%; Score 48; DB 2; Length 20; 100.0%; Pred. No. 1.7;
                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Miljenko
APPLICANT: Weber, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
CORRESPONDENCE: 76
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.3;
                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                   Sequence 48, Application US/08221583 Patent No. 5486595 GENERAL INFORMATION:
                                                    35.0°,
100.0%; Pre-
0;
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO. 48:
SEQUENCE CHARACTERISTICS:
                               Query Match
Best Local Similarity 100.v.
"whas 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.8
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-48
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                     1 PCAPGTFS 8
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US-08-126-01,6-24
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Gaps
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Sequence 58, Application US/09101146
Sequence 58, Application US/09101146
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
OPPRATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: OCCODER 7, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Jane Massey Licata, Esq.
66 E. Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 48:
                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04018
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING COMPANY
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Gaps
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Pred. No. 1.7e+02;
                                                                                        Score 33; DB 1; Length 16; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                              Sequence 141, Application US/08934915

Sequence 141, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: CHENG, HWEE-MING

TITLE OF INVENTION: PAPILLCMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: DIAGNOVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: DIAGNOVIRUS 1, 3, 8, 8,

TITLE OF INVENTION: DIAGNOVIRUS 2, 9, 8,

TITLE OF INVENTION: DIAGNOVIRUS 3, 33 AND 56,

TITLE OF INVENTION: DIAGNOVIRUS 5, 8,

TITLE OF INVENTION: DIAGNOVIRUS 5, 8,

CORRESPONDENCE ADDRESS:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHETIC PEPTIDES OF HUMAN PAPTLLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES
                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: T. S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION OF THE TRANSPORTER OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFRENCE/POCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-493-092-4; Sequence 4, Application US/08493092
                                                                                        24.68;
46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                              5 GTFSNTTSSTDIC 17
                                                                                                                                                                                                                                                2 GTTNNTHCGADFC 14
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                                                                                        Query Match
Best Local Similarity
Matches 6; Conserva
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      US-08-354-618-3
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APPLICANT: Carcia, Blanca Maria Garcia
APPLICANT: Garcia, Blanca Maria Garcia
APPLICANT: Garcia, Emilio Margollez
APPLICANT: Curbelo, Dania Mateu
APPLICANT: Bada, Julio Marcos Delgado
APPLICANT: Martinez, Luis S. Herrera
APPLICANT: Martinez, Jos Alberto Cremata
APPLICANT: Perez-Casta eda, Manuel Rafeel Raices
APPLICANT: Jan nez, Jos Maria Ellena Gonz lez
APPLICANT: Jim nez, Efrain Rodriguez
TITLE OF INVENTION: Dextranase enzyme, method for its
TITLE OF INVENTION: production and DNA encoding the enzyme
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39;
Pred. No.
                                                                                                                                        RAME: Jane Massey Liceta
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELEPHONE: (856) 810-1515
TELEPHONE: (856) 810-1515
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08354618 Patent No. 5637491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 115/93
FILING DATE: 14-December-1993
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ronald J. Baron
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43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 16 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                Lare: Amino Acid
TOPOLOGY: Linear
US-09-101-146-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Campand
APPLICANT: Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-354-618-3
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GENERAL INFORMATION:
APPLICANT: Tagle Danilo A.
APPLICANT: Tagle Danilo A.
APPLICANT: Tagle Danilo A.
APPLICANT: Tagle Danilo A.
APPLICANT: COllins, Francis S.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Relaing, Ethington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STRET: P.O. Box 4390
CITY: Troy
STRET: B.O. Box 4390
CITY: Troy
STRET: B.O. Box 4390
COUNTY: US
COUNTY: US
COUNTY: US
COUNTY: B.O. Box 4390
COUNTY: B.O. Box 4390
COUNTY: B.O. Box 4390
COUNTY: STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CORRENT PRICATION DATA:
APPLICATION NUMBER: US/08/493,092
FILING DATE:
CLASSIFICATION NUMBER: US/08/493,092
FILING DATE:
CLASSIFICATION NUMBER: US/08/493,092
FILING CASSIFICATION NUMBER: 130,955
REFERENCE/DOCKET NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 130,955
REFERENCE/DOCKET NUMBER: 130,955
REFERENCE/DOCKET NUMBER: 130,955
REFERENCE/DOCKET NUMBER: 130,955
REFERENCE/DOCKET NUMBER: 130,055
REFERENCE/DOCKET NUMBER: 130,055
REFERENCE/DOCKET NUMBER: 130,055
REFERENCE/DOCKET NUMBER: 130,055
REGISTRATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid
STRANDENESS: Single
TOPOLOGY: LInear
US-08-493-092-4
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Search completed: February 12, 2002, 13:04:30 Job time: 110 sec

; 0

Gaps

; 0

23.9%; Score 32; DB 1; Length 15; 50.0%; Pred. No. 1.7e+02; Live 3; Mismatches 2; Indels

Query Match 23.9 Best Local Similarity 50.0 Matches 5; Conservative

8 SNTTSSTDIC 17 |::|||:| 6 SSASQSTDLC 15

S G

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2002, 12:54:49; Search time 13.27 Seconds (without alignments) 223.874 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-800-909-2_COPY_163_201 216 1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

8589 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 39

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	T-cell surface qlv	huwentoxin-I - Chi	hypothetical prote	യ	hypothetical prote	agelenin - funnel-	delta-endotoxin -	Ca2+/calmodulin-de	napin large chain	t-complex polypept	somatotropin intro	pheromone precurso	T-cell receptor be	antifungal protein	conceptus protein	dentin matrix, inc	beta-defensin-1 -	T-cell antigen rec	30K allergen - rye	glucagon-like pept	gene HEXA protein	LX-1 tumor antigen	lectin - sunn hemp	Ca2+/calmodulin-de	gene X protein - h		hypothetical prote		homeodomain protei
SUMMAKIES	ΩI	G49050	A37479	S68261	A05323	G82613	A60959	A22977	A42865	S70343	E49410	A60716	A48158	B49048	S28994	C61233	A39830	A45495	S47381	S38292	A60317	I54351	A39269	S08293	B42865	553233	148415	8104	A58589	26
	DB														7															
	Length	37	33	37	39	39	35	30	20	30	34	39	38	18	26	29	35	38	13	16	17	21	22	24	26	31	32	34	18	23
dР	Query	17.8	17.6	15.7	15.5	15.3	15.0		14.4	14.4	٠	14.4	•	•	13.9	•	•	•	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.0	
	Score	38.5	38	3	33.5	33	32.5	32	31	31	31	3	30.5	30	30	30	30	30	29	29	29	29	29	29	29	29	29	29	28	28
	Result No.	-	7	Э	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

•	fibulin 1 variant	antifungal protein	homeotic protein H	metallothionein -	glucagon - Europea	glucagon - bigeye	trypsin inhibitor	1mmunogenic protei	trypsin inhibitor	hypothetical prote	antifungal protein	conotoxin NgVIA -	alpha-Lactalbumin	hypothetical prote	Ig heavy chain V-I	notechis II-5b non	
	2 \$74094	2 \$28995	2 C44636	2 T12330	1 GCFLE	2 A61135	1 TIPU1W	2 A47607	2 S21743	2 E82089	2 S28991	2 A55430	2 PL0164	2 A82208	2 JT0513	2 A39328	
	25	27	27	27	58	53	30	30	31	32	30	31	32	36	36	50	
	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	12.7	12.7	12.7	12.7	12.7	12.5	
	28	28	28	28	28	28	28	28	28	28	27.5	27.5	27.5	27.5	27.5	27	
	30	3.1	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45	

ALIGNMENTS

RESULT 1
 T-cell surface glycoprotein CD8 beta-1 chain, secreted form 5 - human (fragment)
 C. Date: 1. Jan. 1944 #sequence_revision 03-Nov-1995 #text_change 29-Aug-1997
 C,ACCESION: 649030 R;DiSanto, J.P.; Smith, D.; de Bruin, D.; Lacy, E.; Flomenberg, N.
 Eur. J. Immunol. 23, 320-326, 1993 A:Title: Transcriptional diversity at the duplicated human CD8 beta loci.
 A; Reference number: A49050; MUID:93170376
 A;Accession: G49050
 A;Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-37 <dis></dis>
A; Note: sequence extracted from NCBI backbone (NCBIP:125543)
C;Genetics:
A;Gene: GDB:CD8B1; CD8B
A;Cross-references: GDB:119771; OMIM:186730
A; Map position: 2p12-2p12
 C; Keywords: alternative splicing; extracellular protein; glycoprotein
 <pre>Best Local Similarity 34.8%; Pred. No. 2.1e+02; Matches 8; Conservative 5; Mismatches 7; Indels 3; Gaps 1;</pre>
 Qy 1 PCAPGTFSNTTSSTDICRPHQIC 23

1 PCAPGIFSANISSIDICAFAQIC 23 | :| :| :||: | :||: | 13 PLSPNACMDTTA---ILQPHRSC 32 g g

Numbroxin-I - Chinese bird spider
C; Species: Selenocosmia huwena (Chinese bird spider)
C; Species: Selenocosmia huwena (Chinese bird spider)
C; Species: Selenocosmia huwena (Chinese bird spider)
C; Species: Jehang, D: J

A;Accession: JC1089
A;Molecule type: protein
A;Residues: 1-33 <L12>
C;Comment: This peptide is the major active protein component of venom in this specie

Sed

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A;MOlecule rype: DNA
A;Residues: 1-39 <SIM>
A;Cross-references: GB:AE004018; GB:AE003849; NID:g9107093; PIDN:AAF84790.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                              Experimental sources. Servature; Servature, Servature, Servatures. Servatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A60959
R;Hagiwara, K.; Sakai, T.; Miwa, A.; Kawai, N.; Nakajima, T.
Blomed. Res. 11, 181-186, 1990
A;Tille: Complete amino acid sequence of a new type of neurotoxin from the venom of t A;Reference number: A60959
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:2036571
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Agelena opulenta
C.Date: 03-Feb_1994 #sequence_revision 03-Feb-1994 #text_change 24-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Residues: 1-35 <HAG>
C;Keywords: calcium channel inhibitor; presynaptic neurotoxin; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 1.1e+03;
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Pred. No. 1.2e+03;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-endotoxin - Bacillus thuringiensis (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A22977
R; Armstrong, J.L.; Rohrmann, G.F.; Beaudreau, G.S.
J. Bacteriol. 161, 39-46, 1985
A; Reference number: A22977; MUID: 85104736
A; Accession: A22977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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37.5%;
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24 SLSKVTVSADVMRAHR 39
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                     A; Accession: G82613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein gadd7.2 - long-tailed hamster C:Species: Cricetulus longicaudatus (long-tailed hamster) C:Date: OG-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999 C:Accession: S68261 R:Hollander, M.C.; Alamo, I.; Fornace Jr., A.J. R:Hollander, M.C.; Alamo, I.; Fornace Jr., A.J. A;Hollander, Acids Res. 24, 1589-1593, 1996 A;Title: A novel DNA damage-inducible transcript, gadd7, inhibits cell growth, but lacks A;Reference number: S68260; MUID:96211359 A;Accession: S68261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: protein
A.Residues: 1-39 <SOS>
C.Comment: Phospholipases A2 catalyze the calcium-dependent hydrolysis of the 2-acyl grc
C.Superfamily: phospholipase A2
C.Keywords: calcium; carboxylic ester hydrolase; lipid degradation; venom
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N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Heloderma horridum (Mexican beaded lizard)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-Apr-1995
C;Accession: A05323
R;Sosa; B.P.; Alagon, A.C.; Martin, B.M.; Possani, L.D.
Blochemistry 25, 2927-2933, 1986
A;Reference number: A05323; MUID:86243292
A;Note: H. h. horridum
A;Accession: A05323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB2613 ...
hypothetical protein XF1988 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G02613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 37;
                                                                                                                                                    Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
       C; Keywords: presynaptic neurotoxin; venom F; 2-17, 9-22, 16-29/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 2; I
Pred. No. 7.9e+02;
                                                                                                                                         17.6%; Score 38; DB 2;
30.0%; Pred. No. 2.2e+02;
iive 5; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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60.0%;
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A; Residues: 1-37 <HOL>
A; Cross-references: EMBL:L40430
                                                                                                                                                                                     Best Local Similarity 30.0 Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-39 < MOND.
C; Comment: The mRNA encoding this hypothetical protein shows homology at the nucleoti
he complete mRNA encode a protein related to somatotropin through abnormal splici
                                                                                                                                                                                                                                              R;Ronmelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven r A;Reference number: A49410; MUID:94089752
A;Accession: E49410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Somatotropin intron-related protein RDE.25 - rat (fragment)
N.Alternate names: growth hormone gene-related protein RDE.25
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: A60716
R;Montpetit, M.L.; Tenniswood, M.P.
J; Cell. Biochem. 39, 285-292, 1989
A;Title: Does the lack of regression-associated mRNA expression render a rat ventral A;Reference number: A60716; MUID:89214371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pheromone precursor MF alpha - fungus (Filobasidium floriforme)
C;Species: Filobasidialla neoformans, Cryptococcus neoformans
C;Dacte: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: A48158
R;Moore, T.D.; Edman, J.C.
MOI. Cell. Biol. 13, 1962-1970, 1993
A;Fitle: The alpha-mating type locus of Cryptococcus neoformans contains a peptide A;Reference number: A48158; MUID:93180845
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                                                  t-complex polypeptide 1 homolog (peak 2 fraction) - rabbit (fragments)
N;Alternate names: chaperonin homolog (peak 2)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
C;Accession: E49410
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A;Nolecule type: protein
A;Residues: 1-34 *ROM>
A;Residues: 1-34 *ROM>
A;Experimental source: reticulocyte
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIP:141043)
C;Superfamily: molecular chaperone t-complex-type
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38.9%;
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A;Molecule type: nucleic acid
A;Residues: 1-38 <MOO>
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Best Local Similarity
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Ca2+/calmodulin-dependent myosin light chain kinase (autophosphorylation sites)
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C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Sacession: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-Dec-2000
C;Accession: S70343; S70342
R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Blophys. Acta 1295, 34-43, 1996
A;Title: Purlication and sequencing of multiple forms of Brassica napus see A;Reference number: S70340; MUID:96283791
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19;20-24;25-30 <NEU>
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Pred. No. 1.1e+03;
1; Mismatches 9;
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                                                                                                                                                                                                          Score 32; DB 2; 1
Pred. No. 1.2e+03;
6; Mismatches 13;
A;Molecule type: protein
A;Residues: 4.30 <ARM>
C;Superfamily: 28K parasporal crystal protein
C;Keywords: delta-endotoxin
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24.0%;
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llarity 37.5%;
Conservative
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Best Local Similarity 24.0
Matches 6; Conservative
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 4-19 <NE2>
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A;Status: preliminary
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R;Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
R;Fitle: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A;Reference number: A49048; MUID:92387250
A;Accession: B49048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antifungal protein 2 - white mustard (fragment)
(Species: Sinapis alba (white mustard)
() Date: 25.Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
() Accession: 828994
(R:Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, F.FES Lett. 316, 233-240, 1993
(A) Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
(S289899; MUID:93138130)
                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
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C;Species: Felis silvestris catus (domestic cat)
C;Species: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: C61233
R;Thatcher, M:J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; Randal, S.
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                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
A;Note: sequence extracted from NCBI backbone (NCBIN:126064, NCBIP:126070)
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A;Residues: 1-18 <SIO>
A;Experimental source: patient EV, IL-2R+ synovial T-cells
A;Note: sequence extracted from NCBI backbone (NCBIP:113264)
C;Keywords: T-cell receptor
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Matches 5; Conservative
                                                                                   Best Local Similarity 35.7
Matches 10; Conservative
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A;Residues: 1-26 CTER>
C;Superfamily: gamma-thionin
C;Keywords: phosphoprotein
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A;Molecule type: protein
A;Residues: 1-29 <THA>
C;Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I rep
       A;Title: Characterization of fellne conceptus proteins during pregnancy. A;Reference number: A61233; MUID:91198359
A;Accession: C61233
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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-!- FUNCTION: LETHAL NEUROTOXIN. BINDS TO THE NICOTINIC ACETYLCHOLINE
RECEPTOR. BLOCKS NEUROMUSCULAR TRANSMISSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Venom;
MEDLINE-97408601; PubWed-9263120;
Qu Y.-X., Liang S.-P., Ding J., Liu X.-C., Zhang R.-J., Gu X.-C.;
Proton nuclear magnetic resonance studies on huwentoxin-I from the venom of the spider Selenocosmia huwena: 2. Three-dimensional structure in solution...;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94024948; PubMed-8212049;
Liang S.-P., Zhang D.-Y., Pan X., Chen Q., Zhou P.-A.;
"Properties and amino acid sequence of huwentoxin-I, a neurotoxin
purified from the venom of the Chinese bird spider Selenocosmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Blockade of neuromuscular transmission by huwentoxin-I, purified the venom of the Chinese bird spider Selenocosmia huwena.";
                                                                                                                                                                                                                                                                TXHI_SELHU STANDARD; PRT; 33 AA.
P56676; Q9NJC2;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HUWBNTOXIN-I (HWTX-I).
Selenocosmia huwena (Chinese bird spider).
EUKATYOTE; Metazoa; Arthropoda; Chelicerata; Araneae;
Mygalomorphae; Theraphosidae; Selenocosmia.
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P56683
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"Assignment of the three disulfide bridges of huwentoxin-I,
neurotoxin from the spider Selenocosmia huwena.";
J. Protein Chem. 12:735-740(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li M., Zhou Z., Liang S.;
"Huwentoxin-I (HWTX-I) peptide cDNA sequence.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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                       CP23_SPOER
PAP2_SPOEX
PAP3_SPOEX
CAPP_METEX
TX1_SCOGR
RL36_LEPIN
                                                                                                                         TXM2_AGEAP
BD08_BOVIN
                                                                                                              RL36_VIBCH
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MEDLINE-97179771; PubMed-9028007;
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NCBI_TaxID-29017;
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                     100059 seqs, 36664827 residues
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                                                                                              February 12, 2002, 12:56:25
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Maximum Match 100%
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-venom gland;
MEDLINE-20143014; PubMed=10881200;
Wang X. Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
Nicholson G.M., Christle M.J., King G.F.;
"Discovery and characterization of a family of insecticidal
encrotoxins with a rare vicinal disulfide bridge.";
Nat. Struct. Biol. 7:505-513(2000).
                                                                                                                                                                                                                                                                                                                                                          versutus).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
NCBI_TaxID=6904;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR
                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                   J-ATRACOTOXIN-HVIC (J-ACTX-HV1C).
Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.5; DB 1; Length 37; Pred. No. 92; 1; Mismatches 9; Indels
                                                                                                                                                                    Length 33;
                                                                                             Venom; Neurotoxin; Postsynaptic neurotoxin; 3D-structure. DISULFID 2\, 17\,
                                                                                                                                                                                          9; Indels
                                                                                                              22
29
3756 MW; LCCE219FD6D31F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 AA; 3768 MW; E4DDF046CC750FFC CRC64;
                                                                                                                                                                   Score 38; DB 1;
Pred. No. 70;
5; Mismatches
                                                                                                                                                                                                                                                                                                                (Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                     37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venom; Toxin; Neurotoxin; 3D-structure.
DISULFID 3 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                         5.
                                                                        EMBL; AF157504; AAF25774.1; -. PDB; 1QK6; 20-AUG-99.
                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                    17.6%;
30.0%;
                                                                                                                                                                                                             GTFSNTTSSTDICRPHQICN 24
                                                                                                                                                                                                                        | | | :::|:
4 GVFDACTPGKNECCPNRVCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PCAPGTFSNTTSS-TDICR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 PCCPGTSCKAESNGVSYCR 33
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1DL0; PRELIMINARY
                                                                                                                                                       Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                           16
33 AA;
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P822Ž7;
30-MAY-2000 (
30-MAY-2000 (
20-AUG-2001 (
                                                                                                                                                                                                                                                                                  TXJC_HADVE
P82228;
                                                                                                                                                                                                                                                                                                                 30-MAY-2000
20-AUG-2001
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DISULFID
SEQUENCE
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TXJA_HADVE
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                                                                                                                                                                        TISSUE-Venom gland;

MEDLINE=20343014; PubMed=10881200;

Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,

Wang X.-H., Christle M.J., King G.F.;

"Discovery and characterization of a family of insecticidal

neurotoxins with a rare vicinal disulfide bridge.";

Nat. Struct. Biol. 7:505-513(2000).

-! FUNCTION: INSECTICIDAL NEUROFOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLIRE=20343014; PubMed=10881200; Wang X.-H., Connor M., Smith R., Maclejewski M.W., Howden M.E.H., Nicholson G.M., Christle M.J., King G.F.; Nicholson G.M., Christle M.J., King G.F.; Discovery and characterization of a family of insecticidal neurotoxins with a rare vicinal disulfide bridge."; Nat. Struct. Biol. 7:505-513(2000).
                                           versutus).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKaryotí, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; Mygalomorphae; Hexathelidae; Hadronyche.
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J-ATRACOTOXIN-HVIA (J-ACTX-HVIA).
Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 36;
Pred. No. 2.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
D1598B2560BFE997 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
D23A442560B89997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-NUG-2001 (Rel. 40, Last annotation update)
J-ATRACCTOXIN-HVIB (J-ACTX-HVIB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.18;
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83.3%;
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3685 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venom; Toxin; Neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                          NCBI_TaxID=6904;
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3

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13
28
28 AA;
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P56602;
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NON_TER
SEQUENCE
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SEQUENCE
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PPOX_BOVIN
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                                                                                                                                                                                                                                                            -i- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGIVERIDES.
-i- CATALYTIC ACTIVITY: PHOSPHAIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.
-i- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
HYSP: PO0630; 1POC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                  TISSUE-Venom;
MEDLINE-86243292; PubMed-3087412;
Sosa B.P., Alagon A.C., Martin B.M., Possani L.D.;
"Blochemical characterization of the phospholipase A2 purified from the venom of the Mexican beaded lizard (Heloderma horridum horridum
                                                            20-MAR-1987 (Rel. 04, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hagiwara K., Inui T., Nakajima K., Kimura T., Kitada C., Fujino M., Sakakibara S., Nakajima T.; "Agelenin, a spider neurotoxin: determination of the C-terminus as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hagiwara K., Sakai T., Miwa A., Kawai N., Nakajima T.; "Complete amino acid sequence of a new type of neurotoxin from the venom of the spider, Agelena opulenta."; Biomed. Res. 11:181-186(1990).
                                                                                                      Heloderma horridum horridum (Mexican beaded lizard).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eŭkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Agelenidae; Agelena.
NCBI_TaxID=29934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.5; DB 1; Length 39;
Pred. No. 3.3e+02;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         39 AA; 4179 MW; 8F9BC66B5DFB603E CRC64;
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00119; PA2_ASP; PARTIAL.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) AGELENIN.
                             39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 CGAGNAASDYSQLGTEKDTDMCCRDHDHC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                              PRT;
                                                                                                                                                                                                                                       Wiegmann).";
Biochemistry 25:2927-2933(1986).
                                                  20-MAR-1987 (Rel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS, AND AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.0%;
Matches 9; Conservative 3
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001211; PLP_A2.
                             STANDARD;
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                                                                                                                                                  NCBI_TaxID=8552;
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                                                                                              (FRAGMENT).
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                                                                                                                                         Heloderma.
                             PA2_HELHO
P04362;
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NON_TER
SEQUENCE
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                    PA2_HELHO
       RESULT
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MEDLINE-9531315; Pubmed-7607249;

MEDLINE-9531315; Pubmed-7607249;

Taketani S., Yoshinaga T., Furukawa T., Kohno H., Tokunaga R.,

Nishimura K., Inokuchi H.;

"Induction of Leminal enzymes for heme biosynthesis during
differentiation of mouse erythroleukemia cells.";

Eur. J. Biochem. 230:760-765(1995).

-1- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IX TO FORM PROTOPORPHYRIN IX.
-1- CATALYTIC ACTIVITY: PROTOPORPHYRINOGEN-IX + O(2) - PROTOPORPHYRIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- COFACTOR: COMMINS ONE FAD PER HOMODIMER (BY SIMILARITY).
-:- PATHMAX: PENULITIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
-:- POLDHYIN DIOSYNTHESIS; Heme biosynthesis; Oxidoreductase;
amide form, and investigation of the disulfide bond arrangement."; Biomed. Res. 12:357-363(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                              identification of the carboxy-terminus as an amide form.";
Pept. Res. 5:140-144(1992).
-!- FUNCTION: SUPPRESSES THE EXCITATORY POSTSYNAPTIC POTENTIALS
POSSIBLY BY BLOCKING THE PRESYNAPTIC CALCIUM CHANNEL.
PIR: A60959; A60959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                  Sakakibara S.; "Synthesis and disulfide structure determination of agelenin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35;
                                                                                                                                                                       Inui T., Hagiwara K., Nakajima K., Kimura T., Nakajima T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROTOPORPHYRINGEN OXIDASE (EC 1.3.3.4) (PPO) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Venom; Neurotoxin; Calcium channel inhibitor; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
CBE6462825350D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEDFC3F09CB6A345 CRC64;
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Pred. No. 4e+02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                        SYNTHESIS, DISULFIDE BONDS, AND AMIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                MEDLINE-93043890; PubMed-1421801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3825 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CLPHNRFCNALSGP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 CRPH-OICNVVAIP
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18
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AA;
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BD01_BOVIN
P46159;
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                                                                                                           Antibiotic
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                     DISULFID
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                                                                                                                                                                                      Matches
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                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Violaceae; Viola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cyclopsychotride A, a biologically active, 31-residue cyclic peptide isolated from Psychotria longipes.";
J. Nåt. Prod. 57:1619-1625(1994).
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Witherup K.M., Bogusky M.J., Anderson P.S., Ramjit H., Ransom R.W., Wood T., Sardana M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Psychotria longipes.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Rubiaceae; Psychotria
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Pred. No. 5.4e+02;
3; Mismatches 7; Indels
          Indels
                                                                                                                                                                                                                                                                                                               30 AA; 3141 MW; A3D8CA231098E7E7 CRC64;
          5;
 5e+02;
                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYCLOVIOLACIN 01.
Viola odorata (Sweet violet).
                                                                                                                                                                                                                                                                                                                                                                                                                                 CYLA_PSYLO STANDARD; PRT; 31 AA. P56872; P82254; P82254; P82254; P82200 (Rel. 39, Created) PAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) CYCLOPSYCHOTRIDE A (CPT).
                                                                                   30 AA
          Mismatches
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9
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                                                                                    PRT;
 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95230294; PubMed=7714530;
                                                                                                                                                                                                                                                                                                                                         14.48;
37.58;
42.98;
          Conservative
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                    7 CTVTALLGCSCSNRVC 22
                                                                                                                                                                                                                                                                                                                                                                         23 CNVVAIPGNASMDAVC 38
                          38
                                    4 VVVLGGGISGDSLC 17
                          25 VVAIPGNASMDAVC
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=41680;
                                                                                                                                                                                                                                                                                                                                                          . 9
                                                                                   CYO1_VIOOD
P82230;
                                                                                                                                                                                      SEQUENCE
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                                                                  RESULT 8
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Tam J.P., Lu Y.-A., Yang J.-L., Chiu K.-W.;

"An unusual structural motif of antimicrobial peptides containing end-to-end macrocycle and cystine-knot disulfides.";

Proc. Natl. Acad. Sci. U.S.A. 96:8913-8918(1999).

-! FUNCTION: PROBABLY PARTICIPATES IN A PLANT DEFENSE MECHANISM. HAS ANTIBIOTIC ACTIVITY. INHIBITS NEUROTENSIN BINDING. ACTIVE AGAINST BOTH GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.

-!- PTM: THIS IS A CYCLIC PEPTIDE.

-! SIMILARITY: BELONGS TO THE CYCLOTIDE FAMILY.

-! CAUTION: THIS PEPTIDE BEING CYCLIC, ITS SEQUENCE WAS ARBITRARILY CHOSEN TO START AT THE POSITION SHOWN BELOW. AS THE DNA SEQUENCE FROM WHICH IT IS DERIVED IS NOT YET KNOWN, IT IS NOT POSSIBLE TO A ASSIGN THE CORRECT N- AND C-TERMINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 268:6641-6648(1993).
-!- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E.COLI ML35
--- BUT NOT AGAINST S.AUREUS 502A.
--- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
--- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HEREFORD; TISSUE-Neutrophils;
MEDLINE-93203264; PubMed-8454635;
Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
Smith W., Henschen A.H., Cullor J.S.;
"Purification, primary structures, and antibacterial activities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-defensins, a new family of antimicrobial peptides from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 1; Length 31; Pred. No. 7.5e+02; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2e+02;
es 11; Indels
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BY SIMILARITY.

BY SIMILARITY.

ACCOBBB232ED0CD0 CRC64;
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48B872D1025E1A68 CRC64;
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Pred. No. 9.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) BETA-DEFENSIN 1 (BNDB-1); (BNBD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001271; Defensin.
InterPro; IPR001855; Defensin_beta.
Pfam. PF00711; Defensin_beta; 1.
SMART; SM00048; DEFSN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
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01-NOV-1995 (Rel. 32, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.9%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3255 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CTVTALLGCSCKSKVC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 CNVVAIPGNASMDAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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7
15
31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neutrophils.";
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Gaps

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RESULT 11 DIDH_PSESP

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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                 -! - SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Haptophyceae; Isochrysidales; Ochrosphaera.
NCBI_TaxID=35137;
                                                                                                                                                                                                                                                                                                          24 AA; 2614 MW; 80704D8CD9F9BB6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 AA; 3640 MW; 2039BA0FB5710655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 1; 1
Pred. No. 7.9e+02;
2; Mismatches 2;
                                   PIR; 208293; S08293.
HSSP; P04122; 1LGB.
InterPro; IPR000985; Lectin_legA.
InterPro; IPR001220; Lectin_legB.
Pfam; PF00139; lectin_legB: 1.
PROSITE; PS00307; LECTIN_LEGUME_BETA; PARTIAL.
PROSITE; PS00308; LECTIN_LEGUME_ALPHA; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                             13.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ochrosphaera neapolitana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                 Lectin, Glycoprotein.
NON_TER 24 2.
SEQUENCE 24 AA; 265
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Best Local Similarity
Trans 7; Conserve
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6; Conserv?
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1 NLVDIPIPANDDAI
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5 SFSSTKFSTD 14
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P50982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RR2_OCHNE
Q40606;
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SEQUENCE
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RR2_OCHNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oppermenn U.C.T., Maser E.;
"Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl reductase from the gram-negative bacterium Comamonas testosteroni.";
Eur. J. Blochem. 24:744-749(1996).

1- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND 3-0XO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL COMPOUNDS, INCLUDING A METYRAPONE-BASED CLASS OF INSECTICIDES, TO THE RESPECTIVE ALCOHOL METABOLITES.

1- CATALYTIC ACTIVITY: ANDROSTERONE + NAD(P)(+) = 5-ALPHA-ANDROSTANE-3, 17-DIONE + NAD(P)(+).

5-ALPHA-ANDROSTANE-3, 17-DIONE + NAD(P)(+).

1- SUBCELLULAR LOCATION: CYTOPLASMIC.

1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta, Magnollophyta, eudicotyledons; core eudicots; Rosidae, eurosids I; Fabales; Fabaceae; Papillonoideae, Crotalarieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-AUG-1990 (Rel. 15, Last sequence update)
01-FBB-1991 (Rel. 17, Last annotation update)
LECTIN (FRAGMENT).
Crotalaria juncea (Sunn hemp).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foriers A., de Neve R., Strosberg A.D.;
Lectin sequences as a tool for chemotaxonomical classification.";
Physiol. Veg. 17:597-60(1979).
-1- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OVY-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-ALPHA-HYDROXYSFEROLD DEHYDROGENASE (EC 1.1.1.50) (3-ALPHA-HSD)
(HYDROXYPROSTAGLANDIN DEHYDROGENASE) (HSD29) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 4.9e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
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FSNTTSSTDICRPHQICNVVAIPGNASMDAVC 38
                                                                       27
                                                                       FASCHTNGGICLPNR-----CPGHMIQIGIC
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PROSITE; PS00061; ADH_SHORT; PARTIAL.
OXIGOTEGUCTASE; NAD
DOMAIN
6 >15 INVOLVED
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15 AA; 1315 MW;
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66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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P80701;
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P16352;
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RESULT 12 LEC_CROJU

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"Isolation and primary structure of glucagon from the endocrine
pancreas of Thunnus obesus.";
endocrinol. 83:227-232(1991).
-!- AUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
-!- AUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
-!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thunnus obesus (Bigeye tuna).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ectinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidel; Pleuronectidae; Platichthys.
                                                                                                                                                      Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R., Abramson S.N., McIntosh J.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conlon J.M., Davis M.S., Thim L., "Primary structure of insulin and glucagon from the flounder (Platichthys flesus).";
Gen. Comp. Endocrinol. 66:203-209(1987).
                                    ALPHA-CONOTOXIN EI.
Conus ermineus (Atlantic fish-hunting cone).
Eukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 1; Length 18;
Pred. No. 8e+02;
1; Mismatches 5; Indels
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60A61A6C427A6B5E CRC64;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NoV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GLUCAGON.
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                                                                                                                                         MEDLINE-96062516; PubMed=7578057;
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MEDLINE-87219793; PubMed-3556313;
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45.5%;
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3
18
2082 MW;
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Best Local Similarity
Matches 5; Conserv
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P23062;
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GLUC_PLAFE
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09trd4 oryctolagus
09n10 cenorhabdi
077939 human immun
077939 human immun
076030 homo saplen
09hf27 cryptococcu
09hf27 cryptococcu
09t2n6 spinacla ol
09t2n6 spinacla ol
09t2n6 spinacla ol
09t2n6 spinacla ol
09smyl human immun
07805 human immun
03f600 human immun
03f600 human immun
03f610 homo saplen
0911u5 hepatitis c
                                                                                                                                                                                                                                                     09kyn6 streptomyce
09ah14 lactococcus
016368 homo sapien
013254 homo sapien
010486 human immun
                                                                                                                                                                                                                                                                                                                                       Q9qt2 tanapox vir
Q9ur51 filobasidie
Q46711 plasmid r10
Q9wuul mus musculu
073447 human papil
Q9qfaO human immun
   cryptococcu
filobasidie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Komate T., Tsuchiya N., Matsushita M., Tokunaga K.;

Komate T., Tsuchiya N., Matsushita M., Tokunaga K.;

New poliymorphism within the extracellular region of TNFR2.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB030950; BAA89053.1;
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30
3183 MW; 942C00239B909DF5 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CONOTOXIN SCAFFOLD III/IV PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
10-MAY-2000 (TIEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPPOR 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.0%; Score 121; DB 4; I
100.0%; Pred. No. 4.7e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Q9HF26
Q9HDP0
Q9TRD4
Q9N3L0
Q77939
Q76030
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09T2N6
09MZX0
005602
078505
035630
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Q16368
Q13254
O10486
Q9QQT2
Q9UR51
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09KYN6
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090FA0
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                                    3412
                                                                                                                       Conservative
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   NCBI_TaxID=9606;
 Receptor.
NON_TER
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SEQUENCE
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Q9BP43;
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Q9BP43
 AC AC DOT DOT BE REP REP BE RE
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070294 human immun
070294 human immun
070351 human immun
092xh9 bacteriopha
P79330 bos taurus
09bys0 homo sapien
09jex1 cotton leaf
09jex7 rattus sp.
09jex7 xylella fas
09jex7 xylella fas
09jex7 xylella fas
09jex7 xylella fas
09jex7 human adeno
09gl92 human immun
099lp0 human immun
                                                                                                                                      (without alignments)
262.040 Million cell updates/sec
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Ogbp43 conus penna
Ogudb4 homo sapien
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                                                                                                                     February 12, 2002, 12:56:10 ; Search time 21.77 Seconds
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q9UDB4
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Match Length DB
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length: 39
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Maximum DB seq
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of env V3 sequences and their correlation with epidemiologic data.";
           AIDS 8:619-624(1994).
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Matches 10; Conserv
                                   SEQUENCE FROM N.A.
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Best Local Similarity
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Q70294;
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                                                                                                        "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF215130; AAG60535.1;
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MEDLIND=94338597; PubMed=8060542;
Bobkov A.F., Garaev M., Rzhaninova A., Kaleebu P., Pitman R.,
Weber J.N., Cheingsong-Popov R.;
"Molecular epidemiology of HIV-1 in the former Soviet Union: analysis
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MEDLINE-93170376; PubMed-8436166;
DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
Transcriptional diversity at the duplicated human CD8 beta loci.";
Eur. J. Immunol. 23:320-326(1993).
SEQUENCE 37 AA; 3940 MW; 7A4AEIC90IE15E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                         SEQUENCE FROM N.A.
MEDLINE-21105969; PubMed-11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%; Score 38.5; DB 4; Length 37; 34.8%; Pred. No. 2e+02;
             Gastropoda; Caenogastropoda;
                                                                                                                                                                                             5; Length 36;
                                                                                                                                                                                                                     10; Indels
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                                                                                                                                                         36 AA; 3683 MW; 04C74E40FF71141C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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          Eukaryota; Metazoa; Mollusca; Gastropoda
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=37335;
                                                                                                                                                                                             Score 41;
Pred. No. 8
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30.8%;
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
  Conus pennaceus.
                                                                                              Fainzilber M.;
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01-JUN-2000
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SEQUENCE FROM N.A.
MEDLINE=94338597; PubMed=8060542;
MEDLINE=94338597; PubMed=8060542;
Bobkov A.F., Garaev M., Rzhaninova A., Kaleebu P., Pitman R.,
Weber J.N., Cheingsong-Popov R.;
"Molecular epidemiology of HIV-1 in the former Soviet Union: analysis of env V3 sequences and their correlation with epidemiologic data.";
AIDS 8:619-624(1994).
                                                                              Weber J.N.; "Identification of human immunodeficiency virus type 1 subtypes and their distribution in the Commonwealth of Independent States (Former Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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"Identification of human immunodeficiency virus type 1 subtypes and their distribution in the Commonwealth of Independent States (Former Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
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                                Callow D.,
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MEDLINE-93329178; PubMed-8335967;
Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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                           Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Cal.
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                     5C5827FCBD5DB873 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 4.2e+02;
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Pred. No. 4.2e+02;
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EMBL; U10705; AAA19262.1; -
Interpro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
ENVELOPE Protein. 1
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EMBL: U10706; AAA19263.1; -.
Interpro; IPR000777; GP120.
Pfan: PF00516; GP120; 1.
Envelope protein.
MEDLINE-93329178; PubMed-8335967;
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47.6%;
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47.68;
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"Molecular epidemiology of HIV-1 in the former Soviet Union: analysis of env V3 sequences and their correlation with epidemiologic data."; AIDS 8:619-624(1994).
                                                                                                                                                                                                 "Identification of human immunodeficiency virus type 1 subtypes and their distribution in the Commonwealth of Independent States (Former Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of ARI collphage specific to enterohemorrhagic Escherichia coli 0157:H7."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF022930; AAD01756.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Tailed phages; MyovIridae; T4-like phages.
                                                                                                                                        Callow
                                                                                                             MEDIINE-93329178; Pubmed-8335967;
Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Call
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ARI;
Syu W.J., Ding H.C., Seah J.N., Wu K.M., Yu S.L., Tam M.F.,
Chang Y.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 35;
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47.6%; Pred. No. 4.2e+02;
. . . . . . . . . . . . 9; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PUTATIVE VERTEX HEAD SUBUNIT (FRAGMENT).
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Last sequence update)
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EMBL; U10764; AAA19329.1; -
Interpro; IPRO0777; GP120.
Pfam; PF00516; GP120; 1.
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Matches 10; Conserv
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P79330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber J.N.;
"Identification of human immunodeficiency virus type 1 subtypes and their distribution in the Commonwealth of Independent States (Former Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
           Gaps
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MEDLINE=93329178; PubMed=8335967;
Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D., Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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MEDLINE=94338597; PubMed=8060542;
Bobkov A.F., Garaev M., Rzhaninova A., Kaleebu P., Pitman R.,
Weber J.N., Cheingsong-Popov R.;
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Pred. No. 4.2e+02;
0; Mismatches 9; Indels
           Indels
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35
3852 MW; 5C5827FCBD5DBB73 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT)
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01-NOV-1996 (TIEMBLrel. 01, Last Sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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        Mismatches
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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Best Local Similarity 47.69
Matches 10; Conservative
10; Conservative
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SEQUENCE
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Q70295;
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                                                                                    SEQUENCE FROM N.A.
TISSUE-CARTILAGE PROTEOGLYCAN;
MEDLINE-97079270; PubMed-8921002;
Fulop C., Cs-Szabo G., Glant T.T.;
"Species-specific alternative splicing of the epidermal growth factor-like domain 1 of cartilage aggrecan.";
Blochem. J. 319:335-940(1996).
EMBL; L29486; ABB48067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-SCALP;
Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
Rogers M.A., Langbein L., Winter H., Ehman high/ ultrahigh keratin
associated proteins on chromosome 17q12-21.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ406929; CAC27568.1;
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.9e+02;
1; Mismatches 7; Indels
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
AGGRECAN EPIDERMAL GROWTH FACTOR-LIKE DOMAIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 4; Length 33; Pred. No. 7.5e+02;
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                                                                                                                                                                                          SEQUENCE 36 AA; 3614 MW; 9F6C32F15D3BC9DB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KERATIN ASSOCIATED PROTEIN 2.1B (FRAGMENT).
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Last annotation update)
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34.8%;
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Cotton leaf curl virus.
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41.28;
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Matches 8; Conservative
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                                                      Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                        Bos taurus (Bovine).
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01-JUN-2001 (
01-JUN-2001 (
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SEQUENCE
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Q9IEX1;
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Q9QUY5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-GODENDROCYTE-SPECIFIC UDP-GALACTOSE:CERAMIDE GALACTOSYLTRANSFERASE
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Schulte S., Stoffel W.;
Schulte S., Stoffel W.;
Tupp galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins. ?;
Eur. J. Biochem. 233:947-953(1995).
Scholleng IS AA; 1657 MW; 84474749A06BFFCC CRC64;
                                                                                                                                                               Sanz A. I., Fraile A., Garcia-Arenal F., Zhou X., Robinson D.J.,
Khalid S., Butt T., Harrison B.D.;
"Multiple infection, recombination and genome relationships among
begomovirus isolates found in cotton and other plants in Pakistan.";
J. Gen. Virol. 81:839-1849(2000).
EMBL; AJZ70854; CAB97069.1;
InterPro: IPR02488; Gemini_C4.
Pfam: PF01492; Gemini_C4.
Pfam: PF01492; Gemini_C4.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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Pred. No. 7.5e+02;
3; Mismatches 4; Indels
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBL_TaxID=53010;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN XF1988.
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                                                                                                                           STRAIN=P12-IR;
MEDLINE=20318672; PubMed=10859391;
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MEDLINE=96085162; Pubmed=8521863;
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Best Local Similarity 41.7
Matches 5; Conservative
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15 NSNAGTTVLRPH 26
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Best Local Similarity
Matches 6; Conserv
                                                                                             SEQUENCE FROM N.A.
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Xylella fastidiosa
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PGIFXSTTS 10
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NCBI_TaxID=2371;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Characterisation of molecular defects in X-linked amelogenesis imperfecta (AHII).";
Hum. Mutat. 5:251-259(1995).
SEQUENCE 33 AA; 3681 MW; D131F784BD7D8C93 CRC64;
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Pred. No. 1.4e+03;
4; Mismatches 15; Indels
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4501 MW; E085D64BE286D612 CRC64;
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-MAY-2000 (TrEMBLrel. 13, Last sequence update)
-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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                                                         MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95322983; PubMed-7599636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004018; AAF84790.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | | : | |: | 24 SLSKVTVSADVMRAHR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TFSNTTSSTDICRPHQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
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01-MAY-2000 (
01-JUN-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UD12
Q9UD12;
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Q9UD12
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1 PCAPGTFSNTTSSTDICRPHQICNVV 26

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Inda T., Mukoyama A., Yamadera S., Hashido M., Inoue S.;
"Epidemiology and genomic analysis of hexon, fiber and E3 region genes of adenovirus type 7 in Japan.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104382; AAF14124.1;
SEQUENCE 34 AA; 3939 MW; DF8B17CA2DA99972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                             viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 32; DB 12; Length 34; 38.5%; Pred. No. 1.5e+03; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                    34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 12, 2002, 12:59:11 Job time: 181 sec
                                                                                                                                                                                 Created)
                                                                                                                                    PRT;
8 PCSPCRHSHLCLRCSPCSPCLPCFLI 33
                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 7.7 KDA PROTEIN.
                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                          Human adenovirus type 7a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 38.5
Matches 5; Conservative
                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TTSSTDICRPHQI 22
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TTLNHDMAKPHYL 28
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=85755;
                                                                                                                                                                                                                                                                                                Viruses; dsDNA
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S-1058;
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number Minimum DB Maximum DB

Database

Searched:

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Peptide #5868 enco
Peptide #61394 enco
Peptide #6155 enco
Peptide #7028 enco
NF-AT transcriptio
                                                                                                                                                                        | (210/9, 22-329ept
| Hepatitis B surfac
| Hepatiti
                                                                                                                                                                                                                                                                                                                                           Human secreted pro
Human secreted pro
Spacer peptide for
Mu-conotoxin precu
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of synthe Spacer peptide for Human papillomavir Peptide #3373 enco Peptide #3461 enco R1 and R2 peptide R1 and R2 peptide R1 and R2 peptide
                                                                                                                                 Hepatitis B surfac
Antigenic site of
Gene #21 associate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia; cryptic phase; elementary body phase; replicating; probenicid; antiporphyric acid; imune response; infection; diagnostic; assay; MOMP; major outer membrane protein; autoimmune; inflammatory; porphyria; Ebstein Barr virus; antioxidant.
                                                                                                    Human NF-ATcl anti
                                                                                                                     Human NF-AT peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Costant and variable domain sequence of C. psitacci CPS92-106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
             AAW73416
AAM19434
AAM32357
AAM32951
AAM32991
AAY96558
AAY96558
AAW65481
AAW65481
                                                                                                                                                              AAB80444
AAR37510
AAW65475
AAW65476
AAW65479
AAW65480
AAW28490
                                                                                                                                                                                                                                                                                             AAM32087
AAM352087
AAM35518
AAM3551614
AAB27643
AAW44915
AAW44920
AAW41920
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AAM29424
AAM04632
AAU05310
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97US-0045739.
97US-0045779.
97US-0045780.
97US-0045787.
97US-0045787.
97US-0045787.
97US-0045787.
   98WO-US09237
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   Chlamydia psitacci
WO9850074-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1997;
06-MAY-1997;
06-MAY-1997;
06-MAY-1997;
06-MAY-1997;
14-MUG-1997;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1998;
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AAW95323
 ...
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P. pastoris lysyl
Human 5' EST relat
Peptide #3305 enco
Peptide #3392 enco
Peptide #3255 enco
                                                                                                                   (without alignments)
122.565 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 5' EST secre
Human secreted pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Costant and variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  February 12, 2002, 12:54:04; Search time 23.57 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                           // SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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// SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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                                                                                                                                                                                                                                                                                                262775
                                                                                                                                                                                          PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  522463 seqs, 74073290 residues
                                                                                                                                             US-09-800-909-2_COPY_163_201
216
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                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY12433
AAB37394
AAY51973
AAY64941
AAAY64941
AAM16871
AAM29355
AAY24434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95323
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_1101:*
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117
117
228
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225
34
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seq length: 39
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Match
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21.3
19.4
19.0
19.0
18.1
18.1
18.1
118.1
17.4
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Adenovirus hexon Human secreted pr

Score

Result Š 98WO-IB01222.

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31-JUL-1998;
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  Db
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                                                                                                                                                                                                                                              The invention relates to the diagnosis and management of infections by chlamydia species. The invention provides a composition that comprises at least two agents, where each of the agents is effective against a different phase of the chlamydial life cycle. The agents are selected from: (a) agents targetted against clementary body phase of chlamydial life cycle; (b) agents targetted against replicating phase of chlamydial life cycle; (c) agents targetted against replicating phase of chlamydial life cycle; (d) agents targetted against replicating phase of chlamydial life cycle; (d) probenicid, and (e) antiporphyric acid. The composition as used to elicit a protective immune response to Chlamydial infection in an animal or human and is applied until the animal or human tests negative for chlamydia infection. It is also used to treat biological material infected with Chlamydia. Diagnostic kits for antibody assays against recombinant major outer membrane protein (MOMP), and for DNA amplification assays for chlamydial genes, are used to diagnose disease, ceg, autoimmune disease, an inflammatory disease or a disease that occurs in an immuno-compromised individual, associated with Chlamydia and annual and an inflammatory bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample when are also used to detect chlamydial elementary bodies in a sample with character and a season and an and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sample. They are also used to monitor and/or modify the course of therapy in a patient. The treatment reduces the acellular load of infectious Ebstein Barr virus. The method is also used to treat porphyria, by reducing the number of elementary bodies and applying a drug, e.g. cimetidine, and antioxidants, to reduce the adverse effects associated with porphyria. Sequences AAW95320 to AAW95323 represent constant and variable domain sequences of various Chlamydia species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                               Composition with two agents effective against different stages of chlamydial life cycle - comprises agent targetted against cryptic phase, against elementary body phase, against replicating phase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 5' EST secreted protein SEQ ID NO:464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY12433 standard; Protein; 38 AA.
                                                                                                                                                                                                                Claim 4; Fig 3; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.3%;
64.3%;
                                                                                                                                                                          probenicid and antiporphyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1999 (first entry)
                                      Stratton CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
(UYVA-) UNIV VANDERBILT.
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                                                                          WPI; 1999-059653/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 AA;
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                                      Mitchell WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo.sapiens
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinfammatory; antiuleer; vulnerary; antioonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX1004 to AAX41347 repressent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12261 to AAY12314. respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity, the products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                      New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                      B
                                                                                                                                      Duclert A, Dumas Milne Edwards J, Lacroix
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 768-769; 824pp; English
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97US-0905135.
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Best Local Similarity
                                                                                                                                                                                                      WPI; 1999-153778/13.
                                                                                                                                                                                                                                             N-PSDB; AAX41266
                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40200058335-A1.
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01-AUG-1997;
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22-DEC-1999;
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AAY51973
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                                                                                                                                                                                                            human secreted proteins encoded by the genes AAC68081-C68127. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus. Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                                  Nucleic acids encoding human secreted proteins, used to treat, prevent, ameliorate or diagnose conditions such as cancer, and autoimmune diseases e.g. arthritis -
                                                                                                                                                                                                                                                                                                                                                                         (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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41.2%; Pred. No.
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                                                    Komatsoulis G;
                                                                                                                                                                      Claim 11; Page 366; 387pp; English
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         (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
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and parasitic infections.
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                                                    Rosen CA, Ruben SM,
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Matches 7; Conserv
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This invention describes a novel method to manufacture a preparation of an active substance, where the active substance is surrounded by at least one layer consisting of a protein that is cross-linked by an enzyme chosen from the group of lipoxygenase, protein disulfide isomerase, phenol oxidase and peroxidase, lysyl oxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases. Enzymes chosen from lipoxygenase, protein disulfide isomerase, phenol oxidase consulfhydryl oxidases, especially lysyl oxidase are useful for formulation of preparations of active substances. The method of the invention is used for manufacturing preparations of active substances. The preparations are useful as food additives or fodder or as pharmaceuticals. AAY51951-Y51962 represent fragments of the Pichla for manufacturing preparations or sulfacture the method of the consultations or consultation is a pharmaceuticals. AAY51951-Y51962 represent fragments of the pichla for manufacturing preparations or sulfacture the method of the consultation of the pichla consultations.
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Manufacture of active preparations comprises cross linking a protein, which surrounds the active substance with an enzyme, especially a novel lysyl oxidase from Pichia pastoris \,
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                                                                                              Claim 17; Page 17; 22pp; German
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Best Local Similarity 70.0
Matches 7; Conservative
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peroxidases, lysyl oxidases, protein disulfide reductases, tyrosine oxidases or sulfilydryl oxidases is used to formulate compositions containing active ingredients. (I) is useful for crosslinking protein layers surrounding active ingredients in food, animal feed and pharmaceutical products. The compositions can be formulated without using chemical crosslinking agents. AAY51963-Y51974 represent fragments of the Pichia pastoris lysyl oxidase protein which is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
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57;
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Pred. No.
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70.0%;
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N-PSDB; AAZ42555.
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insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent sequences used in the exemplification of the present invention.
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Pred. No. 1.4e+02;
L; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM16871 standard; Protein; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
                                                                                                                                                                                                                                                                                  18.5%;
41.2%;
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                                                                                                                                                                                                                                                                                                                                                                                          2 CAPGTFSNTTSSTDICR 18
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                  28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2.
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
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                                                                                                                                                                                                     Seguence
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AAM29355

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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                          Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenovirus; RGD sequence; adenoviral vector; capsid protein; ligand;
                                                                Peptide #3255 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%; Score 39; DB 22; Length 25,
45.0%; Pred. No. 1.66+02;
7.**Ahas 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenovirus hexon protein heterologous ligand #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID No 13313; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank
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ID AAY24434 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                           2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                (first entry)
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, 'Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AA;
                                                                                                                                                                             WO200157270-A2
                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                             30-JUN-2000;
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                                09-OCT-2001
                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                           26-MAY-2000;
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AAM04573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                Probe;
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                                                                                                                                                                                                                                                                                           Peptide #3392 encoded by probe for measuring placental gene expression.
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                                                  Gaps
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                Length 25;
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Pred. No. 1.6e+02;
                                               Indels
                                                                                                                                                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
               18.1%; Score 39; DB 22; L. 45.0%; Pred. No. 1.6e+02; ive 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 29624; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%; ; 45.0%; I
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2000US-0234687.
2000US-0236359.
                                                                               1 PCAPGTFSNTTSSTDICRPH 20
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2000US-0608408.
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                                                                                                 3 pwfeglpshtttttsimrrh
                                                                                                                                                                                                                                                            (first entry)
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   Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                           AAM29355;
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ID AAM0
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12-MAR-1999;
11-JUN-1999;
03-DEC-1999;
                                                                                                                                                           infections
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                                                                                                                                                                                                                                                   The present invention describes an adenoviral capsid protein comprising a heterologous ligand, where the ligand facilitates binding of the adenovirats to a target cell. The adenoviral vector is used to transfer a transgene to a target cell. The heterologous ligand in the adenoviral capsid protein (especially a fibre or hexon protein or protein IX) adenoviral vector can be used to transfer the human cystic fibrosis transmembrane conductance regulator protein gene to the respiratory epithelium of test animals. The modified adenoviral capsid proteins improve and/or alter the infectious capability of the vector. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive, antiarteriosclerotic; antiaring antipopul, neuroprotective; antiarrhythmic; tranquiliser; vulnerary; antibacterial; antiproratic; antiarrhythmic; antiarrhythmic; antiarrhythmic; antiarrhythmic; antiarrhythmic; antiarrhythmic; cardiovascular disorder; allergic condition; cardiovascular disorder; cancer; neurological disease; tissue repair.
                                                                                                                                                                                                                                                                                                                                                            present sequence represents an adenovirus hexon protein heterologous ligand used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; cytostatic; antiarthritic; antiasthmatic;
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0
                                                                                                                                                                                                   Adenoviral vectors with modified capsid proteins for improved
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39. DB 20. Length 26. Pred. No. 1.7e+02.
2. Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein encoded by gene 35.
                                                                                                                                                           Romanczuk H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB44864 standard; Protein; 34 AA.
                                                                                                                                                                                                                                  Example 1; Fig 1A; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         18.18;
                                                                                                                98US-0071674.
                                                                                             99WO-US00913.
                                                                                                                                                          O'Riordan CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SNTTSSTDICRPHQICNVV 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                               infectious capabilities
                                                                                                                                     (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                              WPI; 1999-444401/37.
                                                                                                                                                                                                                                                                                                                                                                                            26 AA;
                    Mastadenovirus.
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                                                                                                                                                         Armentano D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                  W09936545-A2
                                                                                          15-JAN-1999;
                                                                                                                16-JAN-1998;
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                                                                      22-JUL-1999
infection.
                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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This invention describes a novel isolated polypeptide (I) comprising an amino acid sequence at least 95 % identical to a polypeptide sequences selected from 49 polypeptides encoded by polyuaclectide sequences included in American Type Culture Collection (ATCC) deposit number (C) included in American Type Culture Collection (ATCC) deposit number (C) the condition and in the specification. The products of the invention have (C) transitional cory, neuroprotective, antidiabetic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antidiabetic, cardiant and antidiantacterial, antibsociatic, antidiabetic, candition and for diagnosing a pathological condition or susceptibility (C) antitheumatic, cardiant and anti-HIV activity. (I) or a mucled caid (II) concidition and for diagnosing a pathological condition or susceptibility or the condition. (I) is useful for preventing a disease, disorder or condition affects the activity of the polypeptide and for identifying an activity of in bological sample. (I), (II) or an antibody (IV) specific coil (I) is also useful for treating or preventing a disease, disorder or condition associated with aberrant expression of (I). Diseases treated or diagnosed include immune disorders, such as autoimmune diseases, blood protein associated with aberrant expression of (I). Diseases treated or disponders, anemia, allergic reactions and conditions such as arterioarterial cittude, arrhythmias, arteriosclerosis, coronary thrombosis, organ rejection or graft-versus-host disorders cardiovascular disorders such as arterioarterial figural diseases used associated with increased approsis that include acquired immunodeficiency syndrome (AIDS), corpusis that include acquired immunodeficiency syndrome (AIDS), corpusis that include acquired immunodeficiency syndrome (AIDS), corpusing deto sometic plastic sugery, to treat fibrosis, reperfusion injury or systemic cytokine damage, to stimulate chondrocyte growth, to prevent skin aging due to sunburn, to change a mammal, and produce 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel 49 human secreted proteins useful for diagnosis, prevention and treatment of disorders including neurological, cell proliferative, cardiovascular, and autoimmune/inflammatory disorders and microbial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biology for detecting DNA sequences and as diagnostic probes for detecting the presence of specific mRNA in a particular cell type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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Pred. No. 3.6e+02;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 373-374; 405pp; English.
                                                                                                                                                                                                                                                          Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB51542 standard; Peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
99US-0124142.
99US-0138597.
99US-0168666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%;
33.3%;
                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFSNTTSSTDICRPHQIC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | ::: :|: ||:|
|13 tilniattstlck-hqvc 29
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                                                                                                                                                                                                                                                          Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                  2000-638176/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC79883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
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Homo sapiens
                                                                                                          03-DEC-1998
                                                                                                                                                                                                                                                       29-AUG-1997
                                                                                                                                                                                                                                                                                                        Carter KC,
                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM19434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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• . .
                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to peptides AAB51512 - AAB51537 which represent conserved proteobacterial extracellular domains. Sequences AAB51518 tepresent peptides homologous to YadA, a yersinia adhesin which is an important virulence determinant of the Yersinia species. The invention includes an antibody which binds to the proteobacterial extracellular peptides, and an immunogenic composition containing the antibody used as a vaccine to prevent infection by a proteobacteria. The polypeptides and antibodies are useful in the treatment and prevention of proteobacterial infections. The polypeptides and antibodies are useful in the treatment and prevention of proteobacterial infections. The polypeptides can also be used to identify compounds which antagonize the binding of a bacterial adhesion to its ligand. The host cell can be used to produce the polypeptides in a suitable culture system. The composition can be used to vaccinate a patient against a proteobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                                                                                                                                                                                                                                                                            An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                              Proteobacteria; extracellular domain; virulence determinant; YadA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%; Score 37; DB 21; Length 22; 50.0%; Pred. No. 2.6e+02; ive 1; Mismatches 7; Indels
                                                                                            adhesin; proteobacterial infection prevention; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein encoded by Gene No. 20.
                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 59; 85pp; English.
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                                                                                                                                                                                                                                         BEECHAM CORP.
BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW73416 standard; Protein; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 APGTFSNTTSSTDICRPHQI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-2000; 2000WO-US09866.
                                                                                                                                                                                                                99US-0129073.
                                 15-FEB-2001 (first entry)
                                                         YadA homologous peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                   Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                          WO200061165-A1.
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                                                                                                                                                                  19-OCT-2000
       AAB51542;
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Matches
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Gene No. 20. This sequence represents a human secreted protein, and is expressed ubiquitously, including T-cells and amygdala.

The DNA sequences of the invention and their corresponding secreted protein and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions are diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or astham), hepatic diseases, autoimmune cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is encoded by a cDNA of the invention, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 2.7e+02;
0; Mismatches 9; Indels
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                                                        /note= "unspecified amino acid"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                97US-0044039.
97US-0048093.
97US-0048101.
97US-0048190.
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97US-0050935.
97US-0056250.
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Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ,
Ruben SM, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070209/06.
                       Misc-difference 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                               29-AUG-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
29-AUG-1997;
                                                                                                              WO9854206-A1
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2001WO-US00663

30-JAN-2001;

09-AUG-2001

WO200157272-A2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #6394 encoded by probe for measuring placental gene expression.
                                              Peptide #5868 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                               Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.1%; Score 37; DB 22; Length 27; 83.3%; Pred. No. 3.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 24260; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                            2000us-0180312.
2000us-0207456.
2000us-0608408.
2000us-0632366.
2000us-0224687.
2000us-02345359.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qenetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer.
                                                                                                                         cervical cancer
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phglcn 18
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                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 203-AUG-2000; 21-SEP-2000; 27-SEP-2000; 24-OCT-2000; 2
                                                                                                                                                                          Homo sapiens
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 22; Length 27;
Pred. No. 3.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 32626; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 12, 2002, 12:56:04 Job time: 120 sec
                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.18;
83.38;
                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-023639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                WPI; 2001-488897/53.
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Best Local Similarity
Matches 5; Conserv
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phglcn 18
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                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                           04-FEB-2000;
                                                                                                   30-JUN-2000;
                                                                                      26-MAY-2000;
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Patent No. 5633145

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Mecrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57

CORRESPONDENCES: 57

CORRESPONDENCES: 75

CORRESPONDENCES: 67

STATE: California

COUNTRY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 216; DB 1; Best Local Similarity 100.0%; Pred. No. 3.9e-22; Matches 39; Conservative 0; Mismatches 0;
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US-08-260-174-31
US-09-172-841-7
US-08-944-483-26
US-08-787-091-9
US-08-59-556-7
PCT-US96-05262-12
US-08-444-005-19
US-08-444-005-19
US-08-448-24
US-08-93-314-24
US-08-93-314-24
US-08-93-314-24
US-08-93-314-34
US-08-93-314-34
US-08-93-314-34
US-08-93-314-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: RObblins, Roberta L.
RECISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 51!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ 1D NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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    US-08-050-319B-41
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69.875 Million cell updates/sec
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Patent No. 5395760
Sequence 45, Appl
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                                                                                                                                       ; Search time 12.56 Seconds
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-221-583-46
PCT-US95-04018-46
US-08-221-583-44
PCT-US95-04018-49
PCT-US95-04018-49
PCT-US95-04018-49
US-08-221-583-47
US-08-221-583-48
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-8
PCT-US95-04018-51
US-08-221-583-8
US-08-221-981-3
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US-08-465-982-41
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US-09-037-143-31
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                                                                                                                                                                                                                                                                                                                                                         212252 segs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                     February 12,
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length: 39
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Minimum DB Maximum DB

Database

Total number

Searched:

Perfect score:

Sequence:

OM protein

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Scoring table:

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Gaps

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Score

Result

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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: GEORGESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 1; Length 15; Pred. No. 0.0013; Dred. No. Mismatches 1; Indels
                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   George A.
Tumor Necrosis Factor Inhibitors
                                                                                                                                                 35.6%; Score 77; DB 6; L 100.0%; Pred. No. 0.00029;
                                                                                                                                                              100.0%; Pred ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                        US-08-221-583-45; Sequence 45, Application US/08221583; Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosi
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:10:
5395760-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
93.3%;
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LENGTH: 15 amino acids
                                                                                                                                                                                            Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                     22 ICNVVAIPGNASMDA 36
                                                                                                                                                                                                                                                          1 ICNVVAIPGNASMDA 15
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CLASSIFICATION: 514
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                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 19403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-221-583-46
                                                                                                                                                                                            15;
                                                                                                                                                   Query Match
                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39;
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; APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
                                                                             Sequence 41, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION: P.W. Gray,
APPLICANT: M.Peldmann, P.W. Gray,
TITLE OF INVENTION: Modified human TNFalpha (Tumor; TITLE OF INVENTION: Modified human TNFalpha (Tumor; TITLE OF INVENTION: ADDRESS: 57
CORRESPONDENCE ADDRESS:
ADDRESSE: Reed & Robbins
STREET: 635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Ralease #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
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100.0%; Pred. No. 3.9e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ROBBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIORYAPPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: 405,370
FILINGADATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-Way-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                          STREET: 635 Bryant
CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                94301
                                                              US-08-465-982-41
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5395760-10
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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 5;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                       NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
REFENCE/DOCKET NUMBER: CCOR-0232
TELEPHONE: (215) 568-3100
TELEPAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Liberty Place 46th Floor CITY: Philadelphia
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide PCT-US95-04018-45
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                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
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COUNTRY: US
ZIP: 19403
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CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Macklewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mar. 33,229
REGISTRATION NUMBER: GCOR-0185
REFERENCE/COCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; Length 15;
Pred. No. 0.0013;
0; Mismatches 1; Indels
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APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA
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ZUP: 19403

COMPUTER: READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04018

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/221,580

FILING DATE: O1-APPL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/221,580

FILING DATE: O1-APPL-1994
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                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                       Pennsylvania
: USA
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PCT-US95-04018-45
                                                                                                           COUNTRY:
                                                                CITY: F
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STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCOR-0232
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 568-3100
TELEFRAX: (215) 568-3493
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
 APPLICANT: Weber, Robert W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
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GY: linear
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US-08-221-583-49
                                                                                                                                                                  COUNTRY:
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Patent No. 5466595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                        ;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: B C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
APPLICATION NUMBER: US/08/221,583
FILING DATE:
                                                                                                                                               Score 72; DB 5; Length 15;
Pred. No. 0.0013;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB 1; Length 15;
Pred. No. 0.0018;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT >
PCT-US95-04018-44

CT-US95-04018-44

CENERAL TNFORMATION:
CENERAL TNFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Scor.
100.0%; Pre
                                                                                                                                               33.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                 : 15 amino acids
amino acid
3Y: linear
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                                                                                                                                               Query Match 33.3
Best Local Similarity 93.3
Matches 14; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.9
Best Local Similarity 100.
Matches 14; Conservative
                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-04018-46
                                                                                                                                                                                                                         8 SNTTSSTDICRPHQI 22
                                                                                                                                                                                                                                              1 SNTTSSTDIARPHQI 15
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; MOLECULE TYPE: peptide
US-08-221-583-44
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US-08-221-583-44
                                    TYPE:
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Gaps
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Patent No. 5486595
GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 5; 1
Pred. No. 0.0018;
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Gaps
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595fis
STREET: One Liberty Place 46th Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYZHE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 67; DB 1; Length 15; 86.7%; Pred. No. 0.0062; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                  Length 15
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                                                                                                                                                                                              Score 70; DB 5;
Pred. No. 0.0025;
0; Mismatches 1
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APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-04018-47
Sequence 47, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeLuca, Mark
REGISTRATION UNDHER: 33,229
REPERENCE/DOCKET UNDHER: CCOR
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                32.4%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                            LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-49
    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 amino acids
                                                                                                                                                                                              Query Match 32.4
Best Local Similarity 92.5
Matches 13; Conservative
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CITY: Philadelphia
STATE: Pennsylvania
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Best Local Similarity
Matches 13; Conserv
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ZIP: 19403
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US-08-221-583-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENICAPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 1; Length 15; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNDBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPA: (215) 568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 and no acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION COMBER. FOLLOSSIOUSING
PRIOR APPLICATION DATA:
PRIOR PAPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION UNMBER: US 08/221,581
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-0232
PELECOMNUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
TELEFAX: (215) 568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19403

COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
MAPPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-221-583-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RPHQIANVVAIPGN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 RPHQICNVVAIPGN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DeLuca, Mark
                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04018-49
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STREET: One Liberty Place 46th Floor CITY: Philadelphia
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CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            CCOR-0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 ATTORNEY S14

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: DebLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCC
TELECOMMUNICATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.68;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDIARPHQIANVAI 15
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COUNTRY: USA
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 5; Length 15;
Pred. No. 0.0062;
                 APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                            STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeLuca, Mark
REGISTRATION UNUBER: 33,229
REFERENCE/CDCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM. TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
APPLICANT: Mervic, Miljenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide PCT-US95-04018-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TSSTDIARPHQIANV 15
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                                                                                                                                                                                            Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                        STATE: Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-221-583-48
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Gaps
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SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 1; Length 15;
Pred. No. 0.0084;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
PCT-0595-04018-48
SQUENCE 48, Application PC/TUS9504018
SGENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Mervier, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Search completed: February 12, 2002, 12:56:23 Job time: 114 sec

; 0

0; Gaps

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(without alignments) 326.708 Million cell updates/sec
                                                                                                                                 February 12, 2002, 12:58:45; Search time 13.29 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                      US-09-800-909-2_COPY_201_257
302
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                        Title: .
                                                                                                                                   Run on:
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1 TSTSPTRSMAPGAVHLPQPV......STSFLLPMGPSPPAEGSTGD 219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 57 sed Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

extensin - tomato mucin - sheep (fra neural cell adhesi hypothetical prote dorsal protein - f gpl8 protein - Myc hypothetical prote ATP synthase subun arabinogalactan pr small hypothetical salivary protein P hypothetical prote MHC class I HLA-J sepiapterin reduct hypothetical prote pre-B cell Ig lamb collagen alpha 2(V collagen alpha 1(X troponin T 2fa - r hypothetical prote glycoprotein Ib al cenA protein (IgAl H+-transporting AT H+-transporting AT extensin - tomato mucin, gallbladder Description A60726 S63324 140692 140692 S07073 136139 S16139 S16139 S16137 146522 A37172 A37176 A37170 A37176 A3 Query Match Length DB 56.5 55.5 51 50 47 44.5 44 43.5 43.5 Result Š.

5

Gaps

3;

18.7%; Score 56.5; DB 2; Length 52; 35.7%; Pred. No. 42; ive 4; Mismatches 20; Indels

Query Match
Best Local Similarity 35.7
Matches 15; Conservative

11 SMQYSDIYIPTPTHTHTHT--PHTHTHTHNPNP 49 8 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP

QQ ò

H+-transporting AT gene insl protein

nyosin catalytic

S01945 S51176

53 2 S17672 54 2 S1317 54 2 S1330 55 2 S29770 55 2 S29770 55 2 S29770 57 2 R41715 57 2 T3664 58 2 S24713 59 2 S24713 50 2 J21360 51 2 S24713 51 2 S24713 52 S24713 53 S24713 54 2 S72713 55 2 S24713 56 2 S24713 57 2 R42795		hypothetical prote	kappa-casein - bov	serpin I - horse (DNA-binding protei	autoimmune epitope	neural cell adhesi	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical 3K pr	hypothetical prote	Ig alpha chain, tr	beta-fructofuranos	dihydrolipoamide S	hypothetical prote
0000000000000000	\$17672	C81117	S23202	S14338	S29770	A37238	S25433	T29481	E41715	T36648	JC1360	868260	S24713	S72213	B32040	A82795
	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
	12.9	12.7	12.6	12.6	12.6	12.6	12.4	12.4	12.4	12.4	12.3	12.3	12.3	12.3	12.3	12.3
122 122 122 122 122 123 133 133 133 133	a	ري. دي	38	38	38	38	37.5	37.5	37.5	37.5	37	37	37	37	37	37
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ALIGNMENTS

RESULT 1 AGO 76 B. Adrall 99 C. Species: Bos primigenius taurus (cattle) C. Accession: AGO 76 A. Title: Characterization of bovine gallbladder mucin. Amino ac A. Reference number: AGO 726; MUID: 91007106 A. Residues: 1-54 CAFD> Best Local Similarity 35.2%; Pred. No. 2.3; A Residues: 1-54 CAFD> Best Local Similarity 35.2%; Recensive 6; Mismatches 25; Indels A. Residues: 1-54 CAFD> Best Local Similarity 35.2%; Recensive 6; Mismatches 25; Indels A. Residues: 1-54 CAFD> Best Local Similarity 35.2%; Score 71; DB 2; Length 54; Best Local Similarity 35.2%; Score 71; DB 2; Length 54; Best Local Similarity 35.2%; Pred. No. 2.3; Matches 19; Conservative 6; Mismatches 25; Indels A. Residues: 1-54 CAFD> A. TTTPTVTPLPGSPQTTTPTSSPLPETPTPTSTPPTVPGPSSPQDTEPSGPOPP RESULT 2 Sad 33.4 Byothetical protein YML338w - yeast (Saccharomyces cerevisiae) C. Accession: Sad 33.4 A. Molecule type: DNA A. Reference number: S63 317 A. Residues: 1-52 CABB. A. Residues: 1-52 CABB. A. Residues: 1-52 CABB. A. Residues: 1-53 CABB. A. Residues: 1-53 CABB. A. Residues: 1-54 CABB. A. Residues: 1-55 CABB. A. Cross-references: EMBL: 271614; NID: 91302466; PID: e239576; PID A. Genelicue. A. Reference and Sad 34 A. Genelicue. A	RESULT 1 A60726 mucin, gallbladder - bovine (fragments) C:Species: Bos pringlangenius taurus (cattle) C:Accession: A60726 R:Afdhal, N. H.; Offiner, G.D.; Smith, B.F. A:Afdhal, N. H.; Offiner, G.D.; Smith, B.F. A:Afdersenennant A60726; MulD:91007106 A:Status: preliminary A:Molecule type: protein A:Residues: 1-54 cAFD> A:Molecule type: protein A:Residues: 1-54 cAFD> A:Residues: 1-55 cOBE> A:Resi
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C;Keywords: hydroxyproline
F;6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36022
C;Accession: T36022
Sseger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, March 1999
A;Reference number: 221581
A;Accession: T36022
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $10782
salivary protein P-B - bovine (fragment)
salivary protein P-B - bovine (fragment)
c; Dete: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C; Dete: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C; Accession: $10782
A; Mille: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a A; Mitle: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a A; Mitle: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a A; Miclecance number: $10780; MUID: 90336641
A; Mccession: $10782
A; Molecule type: protein
A; Residues: 1-57 <STR>
C; Superfamily: proline-rich peptide P-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
A;Experimental source: strain A3(2)
(Senetics:
A;Gene: SCOEDB:SCC54.09c
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C:Species: Chenopodium album (lamb's-quarters)
C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S16587
R:Doerfel, P.; Weihe, A.; Dolferus, R.; Boerner, T.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                       2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PRGPYPPGPLAPPOPFG--PGFVPPPPPPPPPGBGR-----IPPPPPAPYGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small hypothetical protein SCC54.09c - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
                                                                                                                                               Length 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2; Leg
Pred, No. 1.7e+02;
                                                                                                                                           Query Match 16.6%; Score 50; DB 2; Le Best Local Similarity 37.1%; Pred. No. 1.4e+02; Matches 13; Conservative 4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.5; DB 2;
Pred. No. 5.3e+02;
2; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                        6 PPAPAPKAPAPAPVPEASTAPVAA--PTTXPSPPA 38
                                                                                                                                                                                                                                                                                              17 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA 51
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Best Local Similarity 28.8%;
Matches 15; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cena protein (IgAlh) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession 140692
R;Miller, Po.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren FEMS Microbiol. Lett. 92, 199-204, 1992
A;Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arabinogalactan protein - Italian ryegrass (fragments)
C;Species: Lolium multiflorum (Italian ryegrass)
C;Date: J-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C;Accession: S07073
R;Gleeson, P.A.; McNamara, M.; Wettenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem, J. 264, 857-862, 1989
A;Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-A;Reference number: S07073; MuID:90147544
A;Accession: S07073
A;Access
                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 267, 10055-10061, 1994
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: S34439; NID: 9249178; PIDN: AAB22153.1; PID: 9249179
C; Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein
C; Keywords: glycoprotein
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                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I70082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-42 <RES>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-25 <RES>
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Pred. No. 60;
1; Mismatches
                                                                                                                                           glycoprotein Ib alpha variant B - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%; Score 55.5; 1
35.6%; Pred. No. 41;
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                                                                                                                                                                                                                                                                                           R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 155355; MUID:92250564
A; Accession: 170082
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Best Local Similarity 46.2%;
Matches 12; Conservative
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Matches 1
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hypothetical protein TCO127 [imported] - Chlamydia muridarum (strain Nigg)
C;Species; Chlamydia muridarum, Chlamydia trachomatis Mopn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: D81737
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
Nucleic Acids Res. 28, 1397-1406, 2000
A;Reference number: A81500; MuID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF39005.1; PID:g719 A;Experimental source: strain Nigg (MoPn) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pre-B cell Ig lambda-like omega light chain (non-rearranging) IGLL2 - human (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 01.Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999
C; Accession: 154515
R; Bauer, T. R.; McDermid, H.E.; Budarf, M.L.; Van Keuren, M.L.; Blomberg, B.B.
Immunogenetics 38, 387-399, 1993
A; Title: Physical location of the human immunoglobulin lambda-like genes, 14.1, 16.1, A; Accession: 154515; MUID:94011089
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collagen alpha 2(V) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-1995
C;Accession: A46662
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                              47
                                                                                               40
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                                                                               VSGLKSHSPPAPHP-TSTSAVCSLTLGP
                                              20 VSTRSQHTQPTPEPSTAPSTSFLLPMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 QPTPEPSTAPSTSFLLPMGPSPPAEGST
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-31 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
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C; Detects 2. Nounce September (Mann)
C; Detects 2. Nounce September (Mann)
C; Detects 2. Nounce September 2. Not (Mann)
E; Messer, G; Zemmour, J; Orr, H.T.; Parham, P.; Weiss, E.H.; Girdlestone, J.
J. Immunol. 148, 4043-4053, 1992
A; Title: HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Implic
A; Reference number: I56139; MUD:92291530
A; Residues: December: I56139
A; Residues: 1-84 CRES.
A; Residues: 1-84 CRES.
A; Residues: 1-28 CRES.
A; Cross-references: GB:M80469; NID:9188483; FIDN:AAA36307.1; PID:9188484
A; Residues: 1-28 CRES.
A; Cross-references: GB:M80469; NID:9188483; FIDN:AAA36307.1; PID:9188484
A; Residues: 1-28 CRES.
A; Cross-references: GB:M80469; NID:9188483; FIDN:AAA36307.1; PID:9188484
A; Rintrons: 24/3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Accession: S32108
R;Maier, J.
Submitted to the EMBL Data Library, March 1993
A;Reference number: S32108
A;Reference number: S32108
A;Reference number: March
A;Residues: 147 < MAI>
A;Residues: 147 < MAI>
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
:Accession: 156139; 172807
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 2; Length 28;
Pred. No. 2.8e+02;
3; Mismatches 10; Indels
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Pred. No. 5.3e+02;
3; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                14.7%; Score 44.5; DB 2; 34.2%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                        16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
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Best Local Similarity 40.9%;
Matches 9; Conservative
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Search completed: February 12, 2002, 13:00:37 Job time: 112 sec
R; Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.
J. Biol. Chem. 268, 9381-9386, 1993
A; Title: Isolation and characterization of the chains of type V/type XI collagen present A; Reference number: A46662; MUID: 93252802
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-39 AMAY
A; Residues: 1-39 AMAY
A; Experimental source: vitreous humor
A; Note: sequence extracted from NCBI backbone (NCBIP:131547)
C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C;Accession. 146522
C;Accession. 146522; MUD: 3.J.; Schachat, F.H.
J. Muscle Res. Cell. Motil. 8, 1-12, 1987
A;Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropc A;Accession: 146522; MUD: 87251333
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A31712
R;Dublet, B.; Van Der Rest, M.
Ann. N. Y. Acad. Sci. 580, 436-439, 1989
A;Title: Comparison between chicken type XII collagen and bovine homologues. A;Title: Comparison between chicken type XII collagen povine homologues. A;Status: preliminary
A;Accession: A37172
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-36 cDUB>
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A;Molecule type: mRNA
A;Rosidues: 1-48 RSRI>
A;Cross-references: EMBL:U04975; NID:g440810; PIDN:AAA16028.1; PID:g440811
C;Superfamily: troponin T
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                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2; Length 39;
Pred. No. 4.8e+02;
0; Mismatches 7; Indels
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Pred. No. 5.4e+02;
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14 LPGPPGPPGEAGPGD 28
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February 12, 2002, 13:00:20 ; Search time 10.05 Seconds
(without alignments)
207.950 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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US-09-800-909-2_COPY_201_257 302 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD Title: Perfect score: Scoring table: Sequence:

57

100059 seqs, 36664827 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

4454 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 57

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	. trirosod	nesct through	P53820 saccharomyc	4	gadus	064211 mycobacteri	O79674 pelomedusa	_		Q9t9d5 paralichthy	_	haloarcul	P26159 rhodobacter				_		P81438 myrmecia gu					Q24395 drosophila	Q9uht9 homo sapien					P12508 human immun		m	Q9mdjl loxigilla n	sus scr	P81728 rattus norv
SUMMAKIES	Ę	4	YN78_YEAST	PRPB_HUMAN	ATP8_GADMO	VG18_BPMD2	ATP8_PELSU	TA6P_HUMAN	MLEV_MOUSE	ATP8_PAROL	FOR2_MYRGU	RPOK_HALMA	YPU3_RHOCA	AP65_CARMA	ATP8_SQUAC	INE1_HUMAN	CA11_RABIT	ATP8_SALAL	FOR1_MYRGU	Y180_TREPA	ATP8_RHEAM	M84C_DROME	H5_COLLI	MTK_DROME	PH68_HUMAN	ATP8_AYTAM	CAPP_METEX	PBAN_LYMDI	ZNT4_BOVIN	TAT_HV1J3	- t	ATP8_CYPCA	읔		SPRT_RAT
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O03168 latimeria c Qyan35 salvelinus P80069 mycobacteri O21401 struthio ca P07448 ratus norv P81247 equisetum a P19755 escherichia P34190 crossostoma P81056 penaeus van P00269 desulfovibr O18417 drosophila			; Saccharomycetes; omyces.	da tabases.	rest rest rent and isb		1; Length 52; 20; Indels 3; Gaps 2; SP 49 il NP 49	AA. te) date) IDE P-A]. Vertebrata; Euteleostomi; ; Hominidae; Homo.
1 ATP8_LATCH 1 ATP8_SALEO 1 A45K_WCBO 1 A45K_WCBO 1 ATP8_STRCA 1 DETS_RAT 1 UCRQ_EOUAR 1 YPC4_ECOLI 1 ATP8_CROLA 1 PEN1_PENVA 1 PEN1_PENVA 1 PURR_DESVH 1 A70A_DROSE 1 CATG_RAT	ALIGNMENTS	ARD; PRT; 52 AA. , Created) , Last sequence update) , Last annotation update) PROTEIN IN COS1 5'REGION.	visiae (Baker's yeast). Ascomycota; Saccharomycotina; Sacc Saccharomycetaceae; Saccharomyces	., Rinke M.; he EMBL/GenBank/DDBJ databases YHR217C.	t. It is proceed to the control of t	; -: / // C1E4066D43E057A1 CRC64	e 56.5; DB . No. 31; ismatches APSTSFLLPMGP 	PRT; 57 quence upda totation up totation up tains: PEPT Craniata; Catarrhini
10.6 55 10.4 10.3 10.3 10.3 10.3 10.1 10.1 55 10.1 55 9.9		STANDARD; (Rel. 34, Cre (Rel. 34, Las (Rel. 40, Las	10170. sa cerevisiae (Baker's 'ungi; Ascomycota; Sac tales; Saccharomyceta	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Subermaler B., Piravandi E., Rinke Submitted (MAY-1996) to the EMBL/(-i - SIMILARITY: TO YEAST YHR217C.	ROT entry is Swiss Instit Swiss Instit Bioinformati Profit inst this stateme puires a licen mail to licen	; CAA96274.1; ; CAA96273.1; 2; YNL338W. protein. 2 AA; 5951 M	al Similarity 35.7%; Pred 15; Conservative 4; M SMAPGAVHLPQPVSTRSQHTQPTPEPST 1 :: SMQYSDIXIPTPTPTHHTHT-PTPHPH-	
34 35 36 37 37 31 31 31 40 41 42 43 30 55 44 30 55 45 45 30 55 45 45 30 55 45 45 30 55 45 45 45 30 31 31 31 31 31 31 31 31 31 31 31 31 31		ULT 1 YNT8 YEAST STANDAR P53820; 01-0CT-1996 (Rel. 34, '01-0CT-1996 (Rel. 34, '01-0CT-1996 (Rel. 40, HYPOTHETICAL 6.0 KDA P	YNL338W OR N0170. Saccharomyces cerev Eukaryota; Fungi; A Saccharomycetales; NCBI_TaxID=4932;	[1] SEQUENCE FRO Obermaier B. Submitted (M	This SWISS- between the the European use by non modified and entities req or send an e	EMBL, 271614; C EMBL, 271613; C SGD; SO005282; Hypothetical pr	Query Match Best Local Simi Matches 15; R 8 SMAPGAV 1 1 SMOYSDI	UMAN UMAN UPAN UPAN UPAN UPAN U-10 U-10 U-10 U-10 U-10 U-10 U-10 U-10
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                                                                                                                                                                                                                                      2;
                       MEDLINE-80006513; PubMed-479131;
Isemura S., Saitoh E., Sanada K.;
"Isolation and amino acid sequences of proline-rich peptides of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johansen S., Bakke I.;
Johansen S., Bakke I.;
Johansen S., Bakke I.;
"The complete mitochondrial DNA sequence of Atlantic cod (Gadus morhua): relevance to taxonomic studies among codfishes.";
Mol. Mar. Biol. Biotechnol. 5:203-214(1996).
-1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBBUNTY) OF THE MITOCHONDIAL ATPASE COMPLEX.
-1- SUBCELLULAR LOCATION: MEMBRANR-BOUND.
-1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NORWEGIAN COASTAL 1; TISSUE-Liver;
MEDLINE-90174958; PubMed=2308841;
Johansen S., Guddal P.H., Johansen T.;
"Organization of the mitochondrial genome of Atlantic cod, Gadus
                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 56
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                                                                                                                                           PEPTIDE P-A. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                               PROLINE-RICH PEPTIDE P-B.
                                                                                                                                                                     2085FBB83BAFD063 CRC64;
                                                             whole saliva.";
D Blochem. 86:79-86(1979).
-1- PTM: P-A IS PROBABLY A DEGRADATION PRODUCT OF PIR; A03297; PJHUSB.
                                                                                                                                                                                                                                                                                                                                                        55 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96414925; PubMed=8817926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gadus morhua (Atlantic cod).
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STRAIN-NORWEGIAN COASTAL 1;
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57 AA;
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             ISSUE-Saliva;
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15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
13.9%; Score 42; DB 1; Length 55; 32.0%; Pred. No. 5.5e+02; iive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%; Score 40; DB 1; Length 51; 33.3%; Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                              4 24 POTENTIAL.
55 AA; 6481 MW; E85C81E63DB48B15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5680 MW; EF85B1AFF5786A34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
NCBI_TaxID=44522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pelomedusa subrufa (African side-necked turtle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGT8_BPMD2 STANDARD; PRT; 51 AA. 064211; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
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                                                                                                                                                                                                                                                                                  16 LPQPVSTRSQHTQPTPEPSTAPSTS 40
                                                                                                                                                                                                                                                                                                               24 LPPKVMAHTEPNEPSPQGMTTPKTA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Biol. 279:143-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF022214; AAC18458.1; -.
                                                                                                                                                                                                         Best_Local Similarity 32.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENE 18 PROTEIN (GP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacteriophage D29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTATP8 OR ATP8
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079674;
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AA.

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EMBL; X12972; CAA31415.1; -.
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                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, S01945; S01945.
HSSP; P04002; 1ATF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                               MYL3 OR MLCIV.
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NON_TER
SEQUENCE
                                                                MLEV_MOUSE
P09542;
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                                                                                                                                                                                                                                                                 (FRAGMENT
KESULT 7 MLEV_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP8_PAROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                   DATE THE PRESENT OF THE PRESENT OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            - FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 4 24 POTENTIAL.
SEQUENCE 55 AA: 6536 MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 39; DB 1; Length 56; 40.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AA; 6535 MW; ACD5D223EEC2C3BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.2%; Score 40; DB 1; I
Best Local Similarity 36.0%; Pred. No. 8.1e+02;
Matches 9; Conservative 3; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TAP2-ASSOCIATED 6.5 KDA POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 HLPQPVSTRSQHTQPTPEPSTAPST 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 HIPNNSPINKKNMLTIPMPWTWPWT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF039066; AAD05054.1; -.
InterPro; IPR001421; ATP-Synt_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF152583; AAD32715.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                 Submitted (DEC-1997) to
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGP_HUMAN
Q9Y3F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Promoter analysis of myosin alkali light chain genes expressed in mouse striated muscle.";
Nucleic Acids Res. 16:10037-10052(1988).
-!- SUBUNIT: MYOSIN IS A HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
-!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS PROTEIN DOES NOT BIND CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Bothidae; Paralichthys.
                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Saitoh K., Hayashizaki K., Yokoyama Y., Asahida T., Toyohara H.,
Yamashita Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
01-MAR-1989 (Rel. 10, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                          STRAIN-C3H; TISSUE-Spleen;
MEDLINE-89057447; PubMed-3194193;
Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
Buckingham M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%; Score 38; DB 1; Length 51; 26.3%; Pred. No. 1.1e+03; ive 6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AA; 5085 MW; CE513ECBA3C8258D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 PQPVSTRSQHTQP--TPEPSTAPSTSFLLPMGPSPPAE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PEPKKDDAKAAAPKAAPAAPAAAPAAAPEPERPKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin; Muscle protein; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paralichthys olivaceus (Flounder). Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                   Submitted (JUN'1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NOMENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
complete nucleotide sequence of Japanese flounder mitochondrial is structural property and cue for resolving teleostean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myrmecia gulosa (Red bulldog ant).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Formicidae; Myrmecilnee; Myrmecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mackintosh J.A., veal D.A., Beattle A.J., Gooley A.A.;
"Isolation from an ant Myrmecia gulosa of two inducible
O-glycosylated proline-rich antibacterial peptides.";
J. Biol. Chem. 273:6139-6143(1998)
-i- FUNCTION: ANTIBACFERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00895; ATP-synt_8; 1. Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. SEOUENCE 55 AA; 6571 MW; 2B5EFEZ0FDCB6AA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 37.5; DB 1; Length 16; 47.1%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1; Length 55; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                  -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-SIMILARITY: TO DROSOPHILA DROSOCIN.
Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
CARBOHYD 1 1 0-LINKED (GALNAC.)
SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BCZE0AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4e+02;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P814s/;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA.
-!- INDUCTION: UPON BACTERIAL CHALLENGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                 IPR001421; ATP-synt_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Hemolymph;
MEDLINE=98165787; PubMed=9497332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LPQPVSTRSQHTQPTPEPSTAPST 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 IPPKVLAHTFPNEPTPOSTOKPKT 47
                                                                                                                                                                                                                                                                                                                         EMBL; AB028664; BAA89037.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.4
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 PQPVSTRSQHTQPTPEP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                       relationship.";
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P81437;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                         Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
NCBI_TaxID=2238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 176:4754-4756(1994).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McKune K., Woychik N.A.; Halobacterial S9 operon contains two genes encoding proteins homologous to subunits shared by eukaryotic RNA polymerases I, II, and III.";
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92105119; PubMed=1840597; MEDLINE=92105119; PubMed=1840597; Kroemer W.J., Arndt E., "Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with genes encoding a tRNA(Leu), the enolase, and putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui."; J. Biol. Chem. 266:24573-24579(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001725; RNA_polk_14KD.
Pfam; PF01192; RNA_pol_K; 1.
PROSITE; PS01111; RNA_POL_K_14KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
MYPOTHETICAL 5.8 KDA PROTEIN IN PUHA 5'REGION (ORF55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D299FDA1954D030F CRC64;
                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
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                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AA.
                              22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94321350; PubMed-8045907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
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Best Local Similarity 42.9
Matches 9; Conservative
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; E41715; E41715
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                              RPOK_HALMA
P29200;
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P26159;
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RPOK_HALMA
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                                  HDDRARD DDRARD D
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SEQUENCE FROM N.A.
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                                    30-MAY-2000 (Rel.
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                                                                               MTATP8 OR ATP8
                                                                                                     Mitochondrion
           ATP8_SQUAC
Q9ZZ50;
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015225;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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INE1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhod@bacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9:
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                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTIBACTERIAL 6.5 KDA PROTEIN (FRACMENT).
Carcinus meenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                              Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 36; DB 1; Length 30; 38.1%; Pred. No. 9.8e+02; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                     Indels
                                                                 Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Photosynthesis; Hypothetical protein.
SEQUENCE 55 AA; 5750 MW; 7EB55296266D48B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 30 30
30 AA; 3305 MW; 6E2C2205934896C4 CRC64;
                                                                                                                                                                                                                                                             Score 36.5; DB 1;
Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        30 AA.
                                                                                                                                                                                                                                                                                                           18 QPVSTRSQHTQPTPEPS--TAPSTSFLLPMGPSP-PA
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97008941; Pubmed-8856051;
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                                                                                                                                                                                                                                                              12.1%;
40.5%;
                                                                                                                                                                                            EMBL; 211165; CAA77517.1; -.
                                                                                                                                                                                                                                                             Query Match 12.1
Best Local Similarity 40.5
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND FUNCTION.
                                                                                                                                                                                                       IR; S17805; S17805.
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Best Local Similarity
Matches 8; Conserv
                                                        SEQUENCE FROM N.A.
                                NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hemocyte;
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NCBI_TaxID=6759;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasmussen A.S., Arrason U.;
"Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes.";
U. Mol. Evol. 48:118-123(1999).
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-!- SUBCELCULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97386586; PubMed-9244435; Esposito T., Gianfrancesco F., Ciccodicola A., D'Esposito M., Nagaraja R., Mazzarella R., D'Urso M., Forabosco A.; Escape from x inactivation of two new genes associated with DXS6974E and DXS7020E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBL_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Homin1dae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
8
                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (AGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. TRANSMEM 6 26 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 26 POTENTIAL.
55 AA; 6587 MW; 3FB9F843CEFA54EE CRC64;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE INACTIVATION ESCAPE 1 PROTEIN (DXS6974E).
AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VILPKKVMTHLFNNNPTAKSAEKPKPEPWNWPWT 55
55
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                      Squalus acanthias (Spiny dogfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99091711; PubMed-9873084;
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                                                                                                    39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y18134; CAA77053.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 43:183-190(1997).
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Forabosco A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS, HEART AND LIVER
FOLLOWED BY BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of rabbit
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PIR; A02856; CGRB1S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONVERTED TO AN ALDEHYDE GROUP THAT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000087; Collagen.
InterPro; IPR001007; VWFC.
PROSITE; PS01208; VWFC; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1; Length 51;
Pred. No. 2e+03;
); Mismatches 8; Indels
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HYDROXYLATION (PROBABLE)
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HYDROXYLATION (PROBABLE)
HYDROXYLATION (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA11_RABIT STANDARD; PRT; 53 AA. 202456; E. U. Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) COLLAGEN ALPHA 1(1) CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-70252720; PubMed-4194291;
                                                                                                       MOSTLY EXPRESSED IN FEMALES
                                                                                                                                                                                                                                                                                                                                                                                                        51 AA; 5425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y10696; CAA71702.2;
MIM; 300164; -.
SEQUENCE 51 AA; 5425 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.6
Best Local Similarity 55.6
Matches 10; Conservative
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SEQUENCE
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Query Match 11.6%; Score 35; DB 1; Length 53;
Best Local Similarity 30.2%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 24; Indels 2; Gaps
Qy 14 VHLPQPVSTRSQHTQPTEPSTAPSTSFLLPMGPSPAEGSTG 56
Db 11 VSVPGPMGPSGPPGLPGPPGAPGP2.GFZGPPG-2PGZPGSSG 51
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3

Search completed: February 12, 2002, 13:03:22 Job time: 182 sec

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014069 homo sapleh
079966 mogurnda ad
071179 chlamydomon
0993p6 human immun
0913t0 homo saplen
0912396 human respi
092319 human respi
092319 human respi
092319 human respi
092310 human respi
092307 human respi
055541 bovine herp
055541 bovine herp
065541 bovine herp
065541 bovine applen
061039 trypanosoma
091039 trypanosoma
091039 trypanosoma
091059 trypanosoma
                                                                                                                                                                                  Q29321 sus scrofa
Q9wtu8 rattus norv
092300 human respi
092311 human respi
                                                                                                                                                                                                   29tsc2 bos taurus
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                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Ishida F.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 1.39103; AAA69491.1; -
Intervo; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
5187. MW; 829FBEB4792EA30F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    016469 PRELIMINARY; PRT; 42 AA. 016469; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) GLYCOPROTEIN IB ALPHA VARIANT B (FRAGMENT).
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.0%; Score 60.5; DB Best Local Similarity 34.7%; Pred. No. 6.9; Matches 17; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                 52 AA
                                                                                                                                                                                                                           ALIGNMENTS
                                       Q41179
Q993P6
Q993T6
Q9WL7E6
Q9WL7E0
Q92310
Q92319
Q92319
Q65541
Q9WA44
                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, Created)
                                                                                                                                     Q9BUX7
061039
Q31629
Q9MYS0
Q29163
Q92317
Q29321
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Q9TSC2
        092311
Q14069
O79966
O79998
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  PRELIMINARY;
  52
52 AA;
   01-NOV-1996
01-NOV-1996
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SEQUENCE
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Q14441;
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Q16469
  RESULT
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09wty7 mus musculu
099138 bos taurus
099768 simian viru
Q15218 homo sapien
018723 macaca fusc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9hb17 homo sapien
Q9gkj3 sus scrofa
Q98m0 solanum tub
Q13697 homo sapien
Q9qu6 drosophila
Q95516 streptomyce
                                                      ; Search time 21.79 Seconds
(without alignments)
382.631 Million cell updates/sec
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092301 human respi
092314 human respi
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Q16469 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                             302
1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD
                                                                                                                                                            33223
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                             473505 segs, 146272329 residues
                                                       February 12, 2002, 13:00:00
                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                      US-09-800-909-2_COPY_201_257
                                        OM protein - protein search, using sw model
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092314
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09GT28
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015218
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Q16469
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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Listing first 45 su
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sp_phage:*
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sp_rodent:*
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length: 57
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143.
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Minimum DB Maximum DB

Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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60.5 55.5 52 51 51

Score

Result Š. 50.5 50.5 49.5 49.5

47.5 47.5 47.5 47

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SEQUENCE FROM N.A.
                            SEQUENCE FROM N.A.
  NCBI_TaxID=11250;
                                          STRAIN-181691;
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SEQUENCE
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                                                                        MEDLINE-92250564; PubMed-1577776; Lopez J.A., Ludwig E.H., McCarthy B.J.; Lopez J.A., Ludwig E.H., McCarthy B.J.; Lopez J.A., Ludwig E.H., McCarthy B.J.; Polymorphism of human glycoproctain to a language of a language of tandem repeats of a 13-amino acid sequence in the mucin-like macroglycopeptide region. Structure/function implications."; J. Blol., Chem. 267:10055-10061(1992).
EMBL: S34439; ABB22153.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-196775;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
"Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF086866, AAC43006.11. -
InterPro; IPR000925; Glycoprot. G.
Pfam: PF00802; Glycoprotein_G; 1.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         Query Match 18.4%; Score 55.5; DB 4; Length 42; Best Local Similarity 35.6%; Pred. No. 20; Matches 16; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxo*iridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                             5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
                                                                                                                                                                                                                                                                                            42 AA; 4222 MW; 228018AC7FBE3F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AA; 5541 MW; 8C3111FE05DF29E0 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-3IN-2001 (TrEMBLrel. 17, Last annotation update)
ATTÄCHMENT GLYCOPROTEIN G (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.2%; Score 52; DB 12; 34.3%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                        52 AA.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequi
01-JUN-2001 (TrEMBLrel.) 17, Last annoi
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
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                                                               SEQUENCE FROM N.A.
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                                       NCBI_TaxID=9606;
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Coggins W.B., Lefkowitz E.J., Sullender W.M.;
"Genetic Variability among Group A and Group B Respiratory Syncytial Viruses in a Children's Hospital.";
Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF086872; AAC42992.1; -
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                         Gaps
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Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Tenetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086888; AAC43008.1;
InterPro; IPR000925; Glycoprot.G.
Pfam; PF00802; Glycoprotein_G; 1.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                     Score 51, DB 12, Length 52, Pred. No. 73, 19; Indels 4, Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Mononegavirales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AA; 5554 MW; 3B328FBC5B4E9858 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                        15 HLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
                                                                                                                                                                                                                                                                                                                                                                                                                        13 HTSQKETLHSTTSEGNPSPSQVYTTSEYLSQSPSP 47
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Pred. No. 73;
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01-JUL-1997 (TrEMBLrel. 04, Last seq
01-JUN-2000 (TrEMBLrel. 14, Last anno
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                                                                                                                                                                                                                                                                                     16.9%;
34.3%;
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31.8%;
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01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Best Local Similarity
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Matches 14; Conserv
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Chung H.Y., Davis M.E., Hines H.C.;
"PCR-SSCP analysis of the bovine calpastatin gene domain L region.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY008267; AAG2869.1; -.
NON_TER 1 1
NON_TER 52 52
SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;
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                                                                                                                                                                                                                                                                                                                                                          0947C8 PRELIMINARY; PRT; 54 AA.
0947C8;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LARGE T ANTIGEN (FRAGMENT);
Simian virus 40 (SV40).
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BEDLINE-BA198116; PubMed-6089212;
Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "SV40 from 1955 commercial parenteral (Salk) poliovaccine.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF180738; AAF28272.1; -. 1
SEQUENCE 54 AA; 5868 MJ. CFC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 54;
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                                                                                                                                                                  DB 6; Length 52;
                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).
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Pred. No. 1.1e+02;
5; Mismatches 25;
                                                                                                                                                                                                     19;
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EMBL; K02578; AAA36505.1; -.
                                                                                                                                                                 Score 50; DB (Pred. No. 94; 3; Mismatches
                                                                                                                                                                                                                                                                5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 37
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32.7%;
                                                                                                                                                                  Ouery Match 16.6%;
Best Local Similarity 33.3%;
Matches 11; Conservative
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Best Local Similarity 32.7
Matches 16; Conservative
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SEQUENCE FROM N.A.
STRAIN-MC-028863B-1;
Rizzo P., Carbone M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10633;
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SEQUENCE
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Q15218;
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                                    SEQUENCE FROM N.A.
MEDLINE=96326790; PubMed=8766138;
MEDLINE=96326790; PubMed=8766138;
MEDLINE=96326790; PubMed=8766138;
Sequence analysis of the GAG triplet repeats region in the Huntington disease gene (IT15) in several mammalian species.";
Ann. Genet. 39:81-86[1996).
EMBL: S83377; AAB50771.1;
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                    Score 50.5; DB 6;
Pred. No. 54;
1; Mismatches 12;
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                                                                                                                                                                                                                                                                                                          16 LPQPVSTRSQHTQP-TPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter.";
Biochim. Biophys. Acta 1443:352-357(1998).
EMBL; AF091262; AAD22613.1; -.
NON_TER 54 54
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV129;
MEDLINE-99096466; PubMed-9878824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 PTPEPSTAPSTSFLLPMGPSPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||| ||: ||
34 PAPEPSQAPA----PPSPTRPA 51
                                                                                                                                                                                                                                    16.7%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, CALPASTATIN (FRAGMENT).
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 11; Conserv
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SEQUENCE FROM N.A.
NCBI_TaxID=9595;
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SEQUENCE
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SEQUENCE
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IPR000925; Glycoprot_G
InterPro; IPR000925; Glycoprot_
Pfam; PF00802; Glycoprotein_G;
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                                              52 AA;
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                                                                                                                                                                                                                                                                                                                                             Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.; ^{\rm A} new repetitive sequence uniquely present in the decay-accelerating
                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-182473;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
"Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086873; AAC42993.1;
                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE SIMILARITY).
                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ;
                    Score 49; DB 4; Length 46;
Pred. No. 1.1e+02;
2; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PPTVQKPTTVNVRTTEVSPTSQKTTTPNAQ----ATRSTPASRTT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ED112B05C37548A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 PGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 49; DB 6;
28.9%; Pred. No. 1.2e+02;
                                                                                                                                                      51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AA
                                                                                   6; Mismatches
                                                                    21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS 54
                                                                                                                                                                                                                                      Macaca fuscata fuscata (Japanese macaque)
                                                                                                                                                                            Created)
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
MEDLINE-98099759; PubMed-9435343;
Nonaka M., Nonaka M., Takenaka O.,
                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 47:246-255(1998).
                                                                                                                                                                          (TrEMBLrel. 08, C
(TrEMBLrel. 08, I
(TrEMBLrel. 08, I
                    Ouery Match 16.2%;
Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
5545 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           (RCA) FAMILY.
EMBL; AB003315; BAA22903.1;
Complement pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                               O18723;
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AA;
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9543;
                                                                                                                                                                                                                                                                                                                                                                    factor genes."
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NON_TER
SEQUENCE
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092302
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Matches
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STRAIN=187701;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (ANG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0868974; AAC42994.1;
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                               Length 52;
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                                                                                                                                               26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pirone D.M., Fukihara S., Gutkind S.J., Burbelo P.D., "SPECS, small binding proteins for CDC42 proteins."; J. Biol. Chem. 0:0-012000).
EMBL, AF286592, AAG17723.1; -.
InterPro; IPR001230; Prenylin.
BPROSITE; PS00349; PRENYLATION; UNKNOWN.1.
SEQUENCE 38 AA; 4245 MW; 3B416F3C5ADF4E91 CRC64;
                                                                                                                                                                                                   49
                                                                                                                                                                                                                               4 TNSTTGNLEHTSQEETLHSTSSEGNTSPSQAYTTSEYLSQPPSP 47
                       C2029E4C5B551270 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09HB17;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                   6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP
                                                                                            Score 49; DB 12;
Pred. No. 1.2e+02;
4; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 49; DB 12; 31.8%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramyxoviridae; Pneumovirinae; Pneumovirus
NCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus.
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                                                                                                 16.2%;
31.8%;
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                                                                                                                                                  14; Conservative
52
5530 I
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                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                   Gaps
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                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
Van Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A.,
Peelman L.J.;
"Integration of porcine chromosome 13 maps.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF222917; AAG41130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                   8;
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Best Local Similarity 36.6%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 14; Indels
Query Match 15.9%; Score 48; DB 4; Length 38; Best Local Similarity 46.7%; Pred. No. 1.2e+02; Matches 14; Conservative 2; Mismatches 6; Indels
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NON_TER 42 42
SEQUENCE 42 AA; 4677 MW; 78BDD867E66EF64F CRC64;
                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN LIGHT CHAIN KINASE (FRAGENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 VHSPQQVDFRSVLAKKGTPKTPVPEKLP-----PPKPTTP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 VHLPQPVSTRS----QHTQPTPEPSTAPSTSFLLPMGPSPP 50
                                                                                                                                                                          42 AA.
                                                             14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLL 43
                                                                                13 VEKPQPVSL-----PTPHPN--PKSSQLL 34
                                                                                                                                                                          PRT;
                                                                                                                                                                        PRELIMINARY;
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Search completed: February 12, 2002, 13:03:05 Job time: 185 sec